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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:00:55 ; Search time 38 Seconds

(without alignment cell updates/sec
1202.762 Million)

Title: US-10-086-156-24

Perfect score: 1780

Sequence: 1 NTMAVLRNRKGGKGPRLRRP.....NNEKSPVQALPAGVFQHPMG 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.101002.*

- 1: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1994.DAT.*
- 16: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1995.DAT.*
- 17: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1996.DAT.*
- 18: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1997.DAT.*
- 19: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	915.5	51.4	271	21	AA15537
2	305	17.1	56	22	ABB28752
3	305	17.1	56	22	ABB33939
4	305	17.1	56	22	ABB19375
5	305	17.1	56	22	AA154702
6	305	17.1	56	22	AA167102
7	305	17.1	56	22	AA14963
8	305	17.1	56	22	AA127397
9	305	17.1	56	22	AA102689
10	305	17.1	56	23	ABG36762

11	282	15.8	190	22	ABG16368	Novel human diapo
12	278	15.6	197	22	ABG73901	Human colton cancer
13	278	15.6	255	22	AAE04891	Human transpore
14	278	15.6	255	23	ABP51810	Human potassium ch
15	278	15.6	258	21	ABP41622	Human ORFX ORF1386
16	245	13.8	175	21	AA153339	Human colton cancer
17	244.5	13.7	130	22	AAW25242	Human protein sequ
18	215	12.1	76	21	AA103290	Human secreted pro
19	214	12.0	146	22	AB11265	Human Edp1 protein
20	211.5	11.9	237	20	AAV34129	Human potassium ch
21	211.5	11.9	237	22	AAU27754	Human full-length
22	211.5	11.9	237	22	AA153682	Human polypeptide,
23	211.5	11.9	237	22	ABP5301	Human polypeptide,
24	211.5	11.9	237	22	ABP5311	Human polypeptide,
25	211.5	11.9	252	23	ABP51311	Human potassium ch
26	206.5	11.6	237	22	AA153832	Human polypeptide,
27	206	11.6	310	22	AA154003	Human stomach can
28	206	11.6	310	22	AA154285	Human protein sequ
29	204	11.5	323	23	AB106073	Human NSI protein s
30	204	11.5	329	22	AA139308	Human polypeptide
31	199.5	11.2	272	22	AA125877	Human protein sequ
32	198.5	11.2	339	22	AA110329	Human transpore
33	196	11.0	301	22	AB10329	Human protein sequ
34	196	10.7	150	23	AB10329	Human protein sequ
35	189.5	10.6	338	22	AB10329	Human protein sequ
36	188.5	10.6	289	20	AB10329	Human protein sequ
37	180.5	10.1	228	22	AB10329	Human protein sequ
38	180	10.1	289	21	AA13411	Drosophila melanog
39	180	10.1	298	21	AA13411	Arabidopsis thalia
40	180	10.1	324	21	AA13409	Arabidopsis thalia
41	180	10.1	396	21	AA13409	Arabidopsis thalia
42	180	10.1	402	21	AA13409	Arabidopsis thalia
43	180	10.1	504	21	AA13409	Arabidopsis thalia
44	180	10.1	707	22	AA13409	Arabidopsis thalia
45	176	9.9	305	22	AA13409	Human polypeptide,

ALIGNMENTS

RESULT 1

ID	AA15537	standard; protein; 271 AA.
XX	AA15537	
AC	AA15537	
XX		
DT	28-FEB-2001	(first entry)
XX		
DE	Human immune system molecule from incyte clone 2751129.	
XX		
KW	Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;	
KW	antiartherosclerotic; antistaphylococcal; antidiabetic; nephrotoxic; cancer;	
KW	antigout; dermatological; antihypertensive; antitumor; hepatotropic; antibac-	
KW	terial; immunosuppressive; cytotoxic; fungicide; protozoicide; antibacterial;	
KW	gene therapy; diagnostic; immunological disorder; viral infection;	
KW	bacterial infection; fungal infection; parasitic infection; immunogen.	
OS	Homo sapiens.	
XX		
PN	MO200060080-A2.	
PD	12-OCT-2000.	
XX		
PF	04-APR-2000; 2000MO-US09072.	
XX		
PR	05-APR-1999; 99US-0127852.	
PR	05-MAY-1999; 99US-0132647.	
XX		
PA	(INCY-) INCYTE PHARM INC.	
XX		
PI	Yue H, Lal P, Tang YT, Baughn KR, Azimzal Y, Lu DM;	
XX		
DR	WPI; 2000-655005/64.	

DR N-PSDB: AAA95776.
XX
PT New human immune system molecules 1-15 and polynucleotides encoding
PT them useful for diagnosing, treating or preventing e.g. immunological
PT disorders, infections, cell proliferative disorders, microbial
PT infections
XX
PS Claim 1; Page 77; 95pp; English.
XX
CC This sequence represents a human immune system molecule (IMOL) encoded
CC by the CDNA isolated as clone 2751129 from the Incyte THPLAZS08 library.
CC The human IMOLs (AA15536-815550) and their encoding polynucleotides
CC (AA95775-895789), and compositions comprising them are useful for the
CC diagnosis, treatment or prevention of immunological disorders,
CC infections and cell proliferative disorders, including cancer. The IMOL
CC may be used to treat or prevent disorders associated with decreased
CC expression or activity of IMOL, such as immunological disorders
CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
CC hematopoietic cancer, infections caused by virus (e.g. adenovirus,
CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
CC disorders (e.g. actinic keratosis, arteriosclerosis, hirsutis), and
CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
CC useful as immunogens for the development of antibodies that
CC specifically recognize these peptides. The polynucleotides may be used
CC to detect and quantify gene expression in biopsied tissues in which
CC expression of IMOL may be correlated with the disease, as targets in a
CC microarray, to detect differences in gene sequences among normal,
CC carrier and affected individuals, and for screening libraries of
CC compounds in drug screening techniques. Antibodies which specifically
CC bind to IMOL may be used for the diagnosis of disorders characterized
CC by expression of IMOL, or in assays to monitor patients being treated
CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
XX
SQ Sequence 271 AA;
Query Match 51.4%; Score 915.5; DB 21; Length 271;
Best Local Similarity 88.0%; Pred. No. 3.3e-74;
Matches 184; Conservative 3; Mismatches 17; Indels 5; Gaps 2;
QY 96 MYYVYGRSDSRROGAMSSSDAEDFLPEATPTAOGHALPLPPEFPEVPLNTGGA 155
DB 1 MYYVYGRSDSRROGAMSSSDAEDFLPEATPTAOGHALPLPPEFPEVPLNTGGA 60
QY 156 HTTTLSTLCRYEDTLMAMFSGRHYIPTDSEGRYFTDRDGTGVDLNFRLSGDLPPRE 215
DB 61 HTTTLSTLCRYEDTLMAMFSGRHYIPTDSEGRYFTDRDGTGVDLNFRLSGDLPPRE 120
QY 216 RYRAVYKKAQYVTAIGPLLEQLENMOPKGEKVRQAFTGLMPYKDHLEIVEIAR-IRAV 274
DB 121 RYRAVYKKAQYVTAIGPLLEQLENMOPKGEKVRQAFTGLMPYKDHLEIVEIAR-IRAV 180
QY 275 QRKA----RFAKIKSLTPEWTLSVLTKMP 299
DB 181 GRPALPSSRSVSSRRCPSPPMVSRSSTP 209
RESULT 2
ID ABB28752
AC ABB28752 standard; Peptide: 56 AA.
XX
AC ABB28752;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1403 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX

PN W0200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes
XX
PS Claim 27; SEQ ID NO 11720; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosis breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 56 AA;
Query Match 17.1%; Score 305; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 FPEVPLNTGGAHFTTTLSTLCRYEDTLMAMFSGRHYIPTDSEGRYFTDRDGTGTF 199
DB 1 FPEVPLNTGGAHFTTTLSTLCRYEDTLMAMFSGRHYIPTDSEGRYFTDRDGTGTF 56
RESULT 3
ID ABB33939
AC ABB33939 standard; Peptide: 56 AA.
XX
AC ABB33939;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #1445 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
KW Homo sapiens.
XX
OS W0200157271-A2.
XX

PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human fetal liver -
 PS Claim 27; SEQ ID NO 26574; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FPEVPLNIGGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 4

ID ABB19375 standard; Protein; 56 AA.

AC ABB19375;

DT 23-JAN-2002 (first entry)

DE Protein #1374 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts -
 PS Claim 15; SEQ ID NO 21145; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FPEVPLNIGGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 5

ID AAM54702 standard; Protein; 56 AA.

AC AAM54702;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26807.

XX Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains -
 XX
 XX Example 4; SEQ ID NO: 26807; 650bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 6
 AAM67102
 ID AAM67102; standard; Protein; 56 AA.

XX
 AC AAM67102;

XX
 DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 27408.

KM Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX
 PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 27408; 658bp + Sequence Listing; English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;

Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 7
 AAM14963
 ID AAM14963; standard; Protein; 56 AA.

XX
 AC AAM14963;

XX 12-OCT-2001 (first entry)

XX Peptide #1397 encoded by probe for measuring cervical gene expression.

KM Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -

XX Claim 27; SEQ ID NO 19789; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGGAHFTTSLTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 8
 AAM27397

ID AAM27397 standard; Protein; 56 AA.
 AC AAM27397;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #1434 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 PS Claim 27; SEQ ID No 27666; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI13135-AI157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SO Sequence 56 AA;
 XX
 XX
 Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 144 FPEVPLNIGAHFTTRLSTLRCEYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAHFTTRLSTLRCEYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
 XX
 RESULT 9
 ID AAM02689 standard; Protein; 56 AA.
 AC AAM02689;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Peptide #1371 encoded by probe for measuring breast gene expression.
 XX
 KW Probe; human; breast disease; breast cancer; development disorder;
 KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200157270-A2.
 XX

PD 09-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US00661.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -
 PS Claim 27; SEQ ID No 11429; 322bp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosis
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer; disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative
 CC breast disease and non-carcinoma tumours.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 56 AA;
 XX
 XX
 Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 144 FPEVPLNIGAHFTTRLSTLRCEYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAHFTTRLSTLRCEYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
 XX
 RESULT 10
 ID ABG36762 standard; Peptide; 56 AA.
 AC ABG36762;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 26427.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.
 PF
 XX 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 DR
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 PS
 XX Claim 27; SEQ ID NO 26427; 634bp; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagazer syndrome, fibrocystic
 CC pulmonary alveolar proteinosis, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 56 AA;
 Query Match 17.1%; Score 305; DB 23; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 144 PEPVPLNIGGAHFTTRLTSTLCYEDTMTAAMSGRRHYITDSEGRFTIDRGTGTF 199
 DB 1 PEPVPLNIGGAHFTTRLTSTLCYEDTMTAAMSGRRHYITDSEGRFTIDRGTGTF 56

RESULT 11
 ABG16368
 ID ABG16368 standard; Protein; 190 AA.
 XX
 AC ABG16368;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #16359.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS80555.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS
 XX Claim 20; SEQ ID NO 46727; 103bp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers, and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 190 AA;
 Query Match 15.8%; Score 282; DB 22; Length 190;
 Best Local Similarity 37.6%; Pred. No. 2.7e-11;
 Matches 71; Conservative 34; Mismatches 66; Indels 18; Gaps 4;
 OY 87 PGARRRGWVVTGREDSRQDGMSSDAEDDELPATPTAQACHALPLQGEPE 146
 DB 5 PGALPLAQVTCMAGCAVE--RPVGSMTSQTPLQSPRPAPRTMS-----T 48
 OY 147 VPLNIGGAHFTTRLTSTLCYEDTMTAAMSGRRHYITDSEGRFTIDRGTGTFGDLNLF 206

Db 49 VTEINVGGEHTTTLGTLRKFPGLKEMSSSLAKASTDAEGRFPIDRPPSTYFRPILDYL 108
 QY 207 RSGCLPREYRAYKRAYAIGLEOLENMPKLGKRY-ROAFLGLMPYKDLERI 265
 Db 109 RTGGV-PTGHPPEYRRAQFEIKPVKLEDMQIFGEVSRQFLQVGYSENLELM 167
 QY 266 VETARLRAY 274
 Db 168 VRLARAEAI 176

RESULT 12
 AAG73901
 ID AAG73901 standard; Protein; 197 AA.
 XX AAG73901;
 AC AAG73901;
 DF 03-SEP-2001 (first entry)
 DE Human colon cancer antigen protein SEQ ID NO:4665.
 XX Human colon cancer antigen protein SEQ ID NO:4665.
 KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KM colorectal carcinoma.
 OS Homo sapiens.
 XX MO200122920-A2.
 PN 05-APR-2001.
 PD 28-SEP-2000; 2000OWO-US26524.
 PF 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI N-PSDB; AAH33332.
 DR N-PSDB; AAH33332.
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 11; Page 6463-6464; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 197 AA;
 SQ Query Match 15.6%; Score 278; DB 22; Length 197;
 Best Local Similarity 39.3%; Pred. NO 6.5e-17;
 Matches 66; Conservative 29; Mismatches 57; Indels 16; Gaps 3;

QY 108 RODGAMSSSDAADDLEPPATPAQGAHALPLLPDPEPVEYVPLNIGAHETTRLSLRCY 167
 Db 12 REVGMTSOTPLPPOSBRPPPTMS-----TWVEINVGGEHTTTLGTLRKF 57
 QY 168 EDTMAAFSSGHNYIPTDESGRYFIDRGTHFGDVNLFPSGLDPLPREYRAYKRAY 227
 Db 58 PCKSLKEMFSSSLAKASTDAEGRFPIDRPPSTYFRPILDYLTGGV-PTGHPPEYRRAQFEI 116
 QY 228 AIGPLEOLENMPKLGKRY-ROAFLGLMPYKDLERIYETARLRAY 274
 Db 117 EIKPLVKLEDMQIFGEVSRQFLQVGYSENLELMVRLARAEAI 164

RESULT 13
 AAE04891
 ID AAE04891 standard; Protein; 255 AA.
 XX AAE04891;
 AC AAE04891;
 DF 10-SEP-2001 (first entry)
 DE Human transporter and ion channel-4 (TRICH-4) protein.
 XX Human transporter and ion channel-4 (TRICH-4) protein.
 KM Human; transporter and ion channel-4; TRICH-4; vaccine; cystic fibrosis;
 KM gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
 KM hypertension; angina; neurological disorder; asthma; bipolar disorder;
 KM dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;
 KM Pick's disease; ischemic cerebrovascular disease; AIDS; anxiety; stroke;
 KM Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
 KM demyelinating disease; mental disorder; schizophrenia; polyomyelitis;
 KM muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
 KM dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
 KM rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
 KM sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
 KM scleroderma; pulmonary artery stenosis; nocturnal; Addison's disease;
 KM malabsorption syndrome; hypercholesterolemia; cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200146258-A2.
 PN 28-JUN-2001.
 PD 22-DEC-2000; 2000OWO-US35095.
 PF 23-DEC-1999; 99US-0172000.
 PR 14-JAN-2000; 2000US-0176083.
 PR 21-JAN-2000; 2000US-0177332.
 PR 28-JAN-2000; 2000US-0178572.
 PR 02-FEB-2000; 2000US-0179758.
 PR 10-FEB-2000; 2000US-0181625.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P,
 PI Hillman JL, Azimzal Y, Yue H, Nguyen DB, Yao MG, Gandhi AR,
 PI Tang YT, Khan FA;
 DR MPI: 2001-418042/44.
 DR N-PSDB; AAD09555.
 XX Novel human transporter and ion channel proteins useful for treating
 PT and preventing transport, neurological, muscle and immunological
 PT disorders -
 XX Claim 1; Page 116-117; 160pp; English.

XX The present sequence is transporter and ion channel-4 (TRICH-4) protein.
 CC TRICH is used as vaccine. TRICH is useful for treating a disease or
 CC condition associated with decreased expression of functional TRICH,
 CC such as transport disorder including amyotrophic lateral sclerosis,
 CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
 CC disease, Duchenne muscular dystrophy, angina and hypertension.

CC neurological disorders including Alzheimer's disease, amnesia, bipolar
 CC disorder, dementia, depression, epilepsy, ischaemic cerebrovascular
 CC disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
 CC disease and Parkinson's disease, demyelinating diseases, mental disorders
 CC including mood, anxiety, schizophrenia and seasonal affective disorder,
 CC muscle disorder including cardiomyopathy, myocarditis, polymyositis,
 CC dermatomyositis, arrhythmias and asthma and immunological disorders
 CC including AIDS, adult respiratory distress syndrome (ARDS), allergies,
 CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
 CC syndrome, systemic lupus erythematosus and other diseases including
 CC sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
 CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
 CC glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
 CC psoriasis and viral, bacterial, fungal, helminthic and protozoal
 CC infections. TRICH DNA is useful in gene therapy and in diagnostic
 CC purposes.

CC Sequence 255 AA;

QY 108 RODGAMSSDAEDDFLEPATPTAOGHMLPLPOEPPEVYPNIGGAHFTRLSTRCY 167
 DB 9 RPYGRMTSQTPLPQSPRRPRTMS-----TYVELNVGGEFTTITGLTRKE 54

QY 168 EDTMLAMFSGRHYIPTDSEGRYFIDRDGTHFGVDVNLFGSDLPFRERAVYKEAOY 227
 DB 55 PGSKLAEMFSSLAKEASTDAEGREFIDRPSYFRPIIDYLRGQV-PQHHPVEYREAOFY 113

QY 228 AIGPILLEENMOPKGEKV-ROAFGLMPYKDHLEIYVETARLAV 274
 DB 114 EIKPLVKLEDMPOIFGQVSRKQFLQVGYSENLEMLVRLARAEL 161

RESULT 14
 AAB51810
 ID AAB51810 standard; Protein: 255 AA.

AC AAB51810;
 XX
 DT 04-OCT-2002 (first entry)

DE Human potassium channel beta-subunit K+beta1 protein SEQ ID NO:2.
 XX
 KW Human; potassium channel beta-subunit; K+beta1; potassium channel;
 KW immunosuppressive; nephrotoxic; neuroprotective; antiinflammatory;
 KW antithyroid; dermatological; cardiant; vasotrophic; anticoagulant;
 KW antidiabetic; cytotatic; vulnary; antibacterial; gene therapy;
 KW antisense therapy; neuronal growth; neuronal damage; neuronal disorder;
 KW neurodegenerative condition; autoimmune disease; inflammatory condition;
 KW hyperproliferative disease; cancer; cardiovascular disorder; infection;
 KW cerebrovascular disease; inflammation; vaccine; lymphatic disease;
 KW angiogenesis; vascular disease.

XX
 OS Homo sapiens.
 XX
 PN WO200248369-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 01-NOV-2001; 2001WO-US50726.
 XX
 PR 02-NOV-2000; 2000US-245366P.
 XX
 PR 21-DEC-2000; 2000US-257851P.
 PA (BRIM) BRISTOL-MTERS SQITB CO.
 PI Feder JN, Lee IM, Chen J, Jackson D, Ramanathan C, Siemers N;
 PI Chang R;
 XX
 DR WPI, 2002-583519/62.

DR N-PSDB; ABO73684.
 XX
 PT Novel human potassium channel beta-subunit, K+beta1 polypeptide and
 PT polynucleotides for diagnosing, prognosing, preventing, treating
 PT immune, hyperproliferative, cardiovascular disorder and for identifying
 PT modulators

PS Claim 33; Fig 1A-B; 316pp; English.

XX
 CC The present sequence represents the human potassium channel beta-subunit
 CC K+beta1 (I). (I) has immunosuppressive, nephrotoxic, neuroprotective,
 CC antithyroid, dermatological, antiinflammatory, cardiant, vasotrophic,
 CC anticoagulant, antidiabetic, cytotatic, vulnary and antibacterial
 CC activities, and can be used in gene therapy and antisense therapy. (I)
 CC can be used for screening candidate compounds (small molecules) capable
 CC of binding to and/or modulating activity of a potassium channel beta-
 CC subunit, by contacting a test compound with a substantially or partially
 CC purified (I) and selecting as candidate compounds those test compounds
 CC that bind to and/or modulate activity of the polypeptide. (I) stimulates
 CC neuronal growth which can be used to treat, prevent, and/or diagnose
 CC neuronal damage which occurs in certain neuronal disorders or neuro-
 CC degenerative conditions. (I) can be used in treating, preventing and/or
 CC diagnosing diseases, disorders or conditions associated with: autoimmune
 CC diseases; inflammatory conditions; hyperproliferative diseases; cancer;
 CC cardiovascular disorders; cerebrovascular disease; inflammation; and
 CC bacterial, fungal or parasitic infection. (I) is also useful as a vaccine
 CC adjuvant that enhances immune responsiveness to an antigen, as a vaccine
 CC to enhance tumour-specific immune responses, anti-viral, anti-bacterial,
 CC anti-fungal, anti-parasitic immune responses. Further (I) is useful as a
 CC stimulator of B cell responsiveness to pathogens, as an activator of T
 CC cells, as an agent to boost immunoresponsiveness among aged populations
 CC and/or neonates, as a stimulator of cytokines, to enhance or inhibit
 CC complement mediated cell lysis, for stimulating wound and tissue repair,
 CC angiogenesis, and the repair of vascular or lymphatic diseases or
 CC disorders.

XX
 SQ Sequence 255 AA;

QY 108 RODGAMSSDAEDDFLEPATPTAOGHMLPLPOEPPEVYPNIGGAHFTRLSTRCY 167
 DB 9 RPYGRMTSQTPLPQSPRRPRTMS-----TYVELNVGGEFTTITGLTRKE 54

QY 168 EDTMLAMFSGRHYIPTDSEGRYFIDRDGTHFGVDVNLFGSDLPFRERAVYKEAOY 227
 DB 55 PGSKLAEMFSSLAKEASTDAEGREFIDRPSYFRPIIDYLRGQV-PQHHPVEYREAOFY 113

QY 228 AIGPILLEENMOPKGEKV-ROAFGLMPYKDHLEIYVETARLAV 274
 DB 114 EIKPLVKLEDMPOIFGQVSRKQFLQVGYSENLEMLVRLARAEL 161

RESULT 15
 AAB41622
 ID AAB41622 standard; Protein: 258 AA.

AC AAB41622;
 XX
 DT 08-FEB-2001 (first entry)

DE Human ORFX ORF1386 polypeptide sequence SEQ ID NO:2772.
 XX
 KW Human; open reading frame; ORFX; detection; cytotatic; hepatotropic;
 KW vulnary; antiparasitic; antiparkinsonian; neurotoxic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarrhythmic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antihelminthic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;

KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

XX 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

PI Shinketsu RA, Leach M;

DR MPI; 2000-602362/57.

DR N-PSDB; AAC75831.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 2011-2012; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;
 CC osteoprotective; anticonvulsant; antiarthritic; immunosuppressive;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antinaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 258 AA;

Query Match 15.6%; Score 278; DB 21; Length 258;

Best Local Similarity 39.3%; Pred. No. 9.6e-17;

Matches 66; Conservative 29; Mismatches 57; Indels 16; Gaps 3;

QY 108 RODAMSSSDAEDDLEPAPPTAQAQHALPLDPEPEVPLNIGAGAFTRRLSTLRXY 167
 DB 12 RPYGRMISQOTPLPSPRRPRPTMS-----TWELNVGGEHHTTLGTRKF 57
 QY 168 EDTMLAAMFSGRHYIPTDSEGRFYIDRDGTHRGVLANFLRSGDLPRRRVRAVKEAGYY 227
 DB 58 PGSKLAKEFSSSLAKASTAEGRFIDRSTYFRPIDYLRKGQV-PTQHIEPVYREAGFY 116
 QY 228 AIGPLLEQLEMMQPKGEKV-RQAFGLMPYTKDLEKRIVEIARLAV 274
 DB 117 EIKPLVYKLEDMPOIFGBOVSKQFLQVPGYSENLEIMVRLARAFAI 164

Search completed: February 12, 2003, 11:07:32
 Job time : 39 secs

APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 258
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-12

Query Match 9.6%; Score 170.5; DB 4; Length 258;
Best Local Similarity 38.9%; Pred. No. 5.3e-09;
Matches 37; Conservative 22; Mismatches 33; Indels 3; Gaps 1;

OY 147 VVPLNIGAHFTRLSTKCYEDTMTLAFSGRHVPTDSEGRYFIDRDGTHGVNFTL 206
DB 34 LMTLVAGGTYLTQKOTLKRYDTELEGIVNGKILCPDADGHTFIDRDLLEFRHYNFL 93
OY 207 RSGDLPPRRVR--AVYKAOYVAGLPLEOLEN 238
DB 94 RNGELLPEGFRENQLAQAEFFOLKGLAEVKS 128

RESULT 3
US-09-166-350-12
Sequence 12, Application US/09166350A
Patent No. 6440663
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Jager, Elke
APPLICANT: Knuth, Alex
TITLE OF INVENTION: Renal Cancer Associated Antigens and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 812
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-350-12

Query Match 9.3%; Score 165; DB 4; Length 812;
Best Local Similarity 33.9%; Pred. No. 1.1e-07;
Matches 43; Conservative 20; Mismatches 60; Indels 4; Gaps 3;

OY 133 GH--ALPLIPQEPPEVVPVPLNIGAHFTRLSTKCYEDTMTLAFSGRHVPTDSEGRYF 191
DB 4 GHGSGPAAAGSGEIVQVNGTSTSRQTLMTIPDSFSSILSGRISTLDEGTGAIF 63
OY 192 IDRDGTHGVNFTLRSGLPPR-ENVRVYKAOYVAGLPLEOLENMGPLGKGVROA 250
DB 64 IDRDPAAPVILNFTLTKELDINGVSNVLRHAEFTYGLTVLRLLCELESSCGSV 123

OY 251 -FLGLMP 256
DB 124 LFHGYLP 130

RESULT 4
US-09-336-643A-14
Sequence 14, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(256)
OTHER INFORMATION: xaa - Any Amino Acid
US-09-336-643A-14

Query Match 8.8%; Score 157.5; DB 4; Length 256;
Best Local Similarity 34.2%; Pred. No. 1e-07;
Matches 40; Conservative 25; Mismatches 47; Indels 5; Gaps 3;

OY 125 PAPTANQAGHALPLPOEPPEVVPVPLNIGAHFTRLSTKCYEDTMTLAFSGRHVPTL 184
DB 10 PASPLXNQ-GIPPAOLTKSNAPVHIDVGHMYTSLSATLTKYESRGRGFDGEPTVL 68
OY 185 DS-EGRYFIDRDGTHGVNFTLRSGLPPRRVR--AVYKAOYVAGLPLEOLEN 237
DB 69 DSLQHYFIDRDGOMERYILNFTLTKSLILPDDRDYTLTYEANYFOLPLLEME 125

RESULT 5
US-09-336-643A-27
Sequence 27, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27
LENGTH: 389
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-27

Query Match 8.6%; Score 153.5; DB 4; Length 389;
Best Local Similarity 34.3%; Pred. No. 5e-07;
Matches 49; Conservative 21; Mismatches 58; Indels 15; Gaps 6;

QY 108 RODGAMSSDAEDDELPAPATQAGHALPLQEPPEVPLINGAHFTTSLKCY 167
DB 57 RDDDVLEVCCEG-PEFIDPQDTSKPEG-----LIGFHDMLTLNNGRYFTTTRSTLVNK 110
QY 168 E-DTMLAAMF--SGRHIPDSEGRYFIDRDGTHFGDVLNLSGDLPRRVR--AYYK 222
DB 111 EPMSTLAKMKKGVWGNKODHRGAFILDSPEYFEPILNLRGQLVNDGINLGYLE 170
QY 223 EAQYATGPLEOLE---NMQP 241
DB 171 EARFEGIDSLIEHLEVAIKNSQP 193

RESULT 6
US-08-606-143-44
Sequence 44, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: LI, MIN
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-44

Query Match 7.8%; Score 138; DB 2; Length 162;
Best Local Similarity 37.3%; Pred. No. 4.6e-06;
Matches 41; Conservative 19; Mismatches 45; Indels 22; Gaps 4;
QY 146 EYVPLINGAHFTTSLKCYEDTMLAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLN 205
DB 2 EYLVVNVSGRHFETWKNLTDRYPTLIGS--SEKEFFDASGEYFFDRDPMFRHYLNF 59

QY 206 LNSGDL--PPRRVAVYKEAQYATGPLEQ---LENNQPLGKERYQAFGLAMPYKD 260
DB 60 YATGRHCHRCQICQAFDELAIFYGLPELVBCCEFFRDR-----KE 104
QY 261 HIERVE 267
DB 105 NAERLAE 111

RESULT 7
US-09-336-643A-10
Sequence 10, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 646
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(646)
OTHER INFORMATION: Xaa - Any Amino Acid
US-09-336-643A-10

Query Match 7.5%; Score 133.5; DB 4; Length 646;
Best Local Similarity 29.9%; Pred. No. 0.00011;
Matches 44; Conservative 19; Mismatches 51; Indels 33; Gaps 5;

QY 137 LPLPQEP-----EYVPLINGAHFTTSLKCYEDTMLAMFSGRHYIPTD 185
DB 20 LPPAQOPLPAPGVKASRGDXVLVNVSGRHFETWKNLTDRYPTLIGS--SEKEFFYDA 77
QY 186 SEGRYFIDRDGTHFGDVLNLSGDL--PPRRVAVYKEAQYATGPLEQ---LENNQ 240
DB 78 DSGRYFIDRDGTHFGDVLNLSGDL--PPRRVAVYKEAQYATGPLEQ---LENNQ 137
QY 241 PLKGEVROAFGLAMPYKHIERVE 267
DB 138 DRK-----KEMERLAE 149

RESULT 8
US-09-142-791A-2
Sequence 2, Application US/09142791A
Patent No. 6368823
GENERAL INFORMATION:
APPLICANT: Antoine Michel Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Fatvre
APPLICANT: Jean-Luc Javre
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02

PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-2

Query Match 7.1%; Score 127; DB 4; Length 636;
Best Local Similarity 34.7%; Pred. No. 0.00047;
Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

QY 137 LPILP-----QEPPEVVPINIGAHFTTRSLTLCYEDTMTAMFSGRHHYIPDSEGRYFI 192
DB 27 MFLPADKRRKRODELIVLVNSGRFRQWTTLERYPTLLGS--TEKEFFENEDTKREYFF 84
193 DRDGTFFGVDVNLFRSGDL--PPREVRVAYYKEAOYYAIGP 231
DB 85 DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGIILP 125

RESULT 9
US-09-178-109-4
Sequence 4, Application US/09178109
Patent No. 6395477

GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Hual-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/09/178,109
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: human
US-09-178-109-4

Query Match 7.1%; Score 127; DB 4; Length 636;
Best Local Similarity 34.7%; Pred. No. 0.00047;
Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

QY 137 LPILP-----QEPPEVVPINIGAHFTTRSLTLCYEDTMTAMFSGRHHYIPDSEGRYFI 192
DB 27 MFLPADKRRKRODELIVLVNSGRFRQWTTLERYPTLLGS--TEKEFFENEDTKREYFF 84
193 DRDGTFFGVDVNLFRSGDL--PPREVRVAYYKEAOYYAIGP 231
DB 85 DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGIILP 125

RESULT 10
US-09-142-791A-4
Sequence 4, Application US/09142791A
Patent No. 6368823

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Falvire
APPLICANT: Jean-Luc Javre

APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 655
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-4

Query Match 7.1%; Score 127; DB 4; Length 655;
Best Local Similarity 34.7%; Pred. No. 0.00049;
Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

QY 137 LPILP-----QEPPEVVPINIGAHFTTRSLTLCYEDTMTAMFSGRHHYIPDSEGRYFI 192
DB 27 MFLPADKRRKRODELIVLVNSGRFRQWTTLERYPTLLGS--TEKEFFENEDTKREYFF 84
193 DRDGTFFGVDVNLFRSGDL--PPREVRVAYYKEAOYYAIGP 231
DB 85 DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGIILP 125

RESULT 11
US-09-178-109-2
Sequence 2, Application US/09178109
Patent No. 6395477

GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Hual-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/09/178,109
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 655
TYPE: PRT
ORGANISM: human
US-09-178-109-2

Query Match 7.1%; Score 127; DB 4; Length 655;
Best Local Similarity 34.7%; Pred. No. 0.00049;
Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

QY 137 LPILP-----QEPPEVVPINIGAHFTTRSLTLCYEDTMTAMFSGRHHYIPDSEGRYFI 192
DB 27 MFLPADKRRKRODELIVLVNSGRFRQWTTLERYPTLLGS--TEKEFFENEDTKREYFF 84
193 DRDGTFFGVDVNLFRSGDL--PPREVRVAYYKEAOYYAIGP 231
DB 85 DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGIILP 125

RESULT 12
US-09-142-791A-6
Sequence 6, Application US/09142791A
Patent No. 6368823

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Falvire
APPLICANT: Jean-Luc Javre

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Falvay
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rounet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-6

Query Match 6.7%; Score 120; DB 4; Length 636;
Best Local Similarity 27.0%; Pred. No. 0.0023;
Matches 40; Conservative 22; Mismatches 44; Indels 42; Gaps 6;

QY 137 LPLP---OEPEVVPVLTGNAHFTTTLSTLCYEDTMTLAAFGSHHYIPTDSEGRYI 192
DB 27 MFLAPADKNRODELILYANSGRFOTWRTLTERTPTLLGS--TEKEFFENEDEKEYFF 84
QY 193 DRDGTGHDVNLRLSGDLPERRRVRVYEAQYATGPLELQENNOPLKGEVROAFL 252
DB 85 DRDPEVFRCLVNRFGKL-----HYTRCISAYDEL-----AFY 121
QY 253 GLMP-----YKRD-----HLRIIVE 267
DB 122 GLPEITIGDCYEYDRKRENERLMD 149

RESULT 13
US-08-606-143-45
Sequence 45, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: LI, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-45

Query Match 6.7%; Score 119.5; DB 2; Length 159;
Best Local Similarity 28.7%; Pred. No. 0.00031;
Matches 39; Conservative 14; Mismatches 44; Indels 39; Gaps 4;

QY 147 VVPLNIGAHFTTTLSTLCYEDTMTLAAFGSHHYIPTDSEGRYIFDRDGTGHDVNL 206
DB 3 LIVLVSGTRQWQDTERYPDTLLGS--SERDEFYHBEPTQOYFDRDPDIFRHLTFY 60
QY 207 RSGDLPERRRVRVYEAQYATGPLELQENNOPLKGEVROAFLGLMP-----Y 257
DB 61 RGLHYPRHECISAYDE-----ELAFGLPEITIGDCYEE 96
QY 258 YKD---HLRIIVEIA 269
DB 97 YKDRRENERLQDDA 112

RESULT 14
US-08-470-335-188
Sequence 188, Application US/08470335F
Patent No. 6147190
GENERAL INFORMATION:
APPLICANT: GOODEBAR, ANDREW
APPLICANT: STROOBART, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/00200B
CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 188
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-08-470-335-188

Query Match 6.1%; Score 108.5; DB 4; Length 349;
Best Local Similarity 23.5%; Pred. No. 0.013;
Matches 70; Conservative 33; Mismatches 98; Indels 97; Gaps 14;

QY 9 RRGGRGPLRRPLA-----LPALRLGELPNQGTSAASAGSGRRSGCAPAGREVRGV 61
DB 9 RRGGRGPLRRPLA-----LPALRLGELPNQGTSAASAGSGRRSGCAPAGREVRGV 58
QY 62 ECATLPAHHCSPBSGCAAGRVMPGAARRANGVYVYGRDSDRSGDAMS----- 114
DB 59 -----ASVCYSSP-----BSVGSVDELAQRAA---VVEEGKVHPORROCALPKRAAAA 105
QY 115 -----SSDAEDDFLE-----PATPAT-----QAGHALPLPQEF 144
DB 106 GAGANGGDRPPAAGPRLGPPAEPLLAANGTVSWPTAPVPSAGPEGEAPYL-VKV 164

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:04:55 / Search time 14 Seconds

(without alignments)
1016.170 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780
Sequence: 1 MTMAVLRNRKRGKGLRRRRP.....NNEKKSPVQLPAGVFQHFNG 343

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	9.8	316	TNPL_HUMAN	Q13829 homo sapien
2	151	8.5	265	Y176_HUMAN	Q14681 homo sapien
3	123	6.9	460	MYCN_HUMAN	Q61976 marimota mon
4	122.5	6.9	601	C1K5_MUSPF	P79197 mustela put
5	121	6.8	490	C1K1_DROME	P17971 drosophila
6	121	6.8	602	C1K5_MOUSE	Q61762 mus musculu
7	119.5	6.7	613	C1K5_HUMAN	P22460 homo sapien
8	113.5	6.4	602	C1K5_RAT	P19024 ratius norv
9	112	6.3	2517	NCR2_HUMAN	Q9Y618 h nuclear r
10	110	6.2	598	C1K5_RABIT	P50638 cycocolagus
11	106.5	6.0	525	C1K3_RAT	P15384 ratius norv
12	106.5	6.0	656	C1K5_DROME	P08510 drosophila
13	105.5	5.9	464	MYCN_HUMAN	P04198 homo sapien
14	105.5	5.9	825	SE5_RAT	P63003 ratius norv
15	105	5.9	499	C1K2_DROME	P16389 homo sapien
16	104.5	5.8	985	C1K2_DROME	P17970 drosophila
17	103.5	5.8	757	C1K3_MOUSE	Q14003 homo sapien
18	101.5	5.7	294	NUGC_MOUSE	P08600 mus musculu
19	101	5.7	499	C1K2_MOUSE	P15386 mus musculu
20	101	5.7	528	C1K3_MOUSE	P16389 mus musculu
21	101	5.7	740	GAG_SMRVH	P12141 squitrel mo
22	101	5.7	960	EGDI_MOUSE	P52734 mus musculu
23	100.5	5.6	523	C1K3_HUMAN	P22001 homo sapien
24	100.5	5.6	1319	MNL_HUMAN	Q10571 homo sapien
25	100	5.6	493	C1K1_MOUSE	P16388 mus musculu
26	100	5.6	495	C1K1_RAT	P10499 ratius norv
27	100	5.6	1411	TCOR_HUMAN	P13448 homo sapien
28	99	5.5	495	C1K1_HUMAN	Q09470 homo sapien
29	98	5.5	356	Y429_HUMAN	Q43312 homo sapien
30	98	5.5	361	EGDI_HUMAN	P98174 homo sapien
31	97	5.4	499	C1K2_XENTLA	P22739 xenopus lae
32	97	5.4	960	SMGC_RAT	Q9W13 ratius norv
33	97	5.4	993	ROXN_HUMAN	Q9UG12 homo sapien

34	96	5.4	529	C1K6_HUMAN	P17658 homo sapien
35	96	5.4	1238	BVGS_BORPA	P40330 bordetella
36	95	5.3	889	C1K6_RAT	P01956 ratius norv
37	95	5.3	2175	HMCU_DROME	P10180 drosophila
38	94.5	5.3	365	HK61_RAT	Q35762 ratius norv
39	94.5	5.3	2167	SHR1_RAT	Q9W448 ratius norv
40	94	5.3	367	HK61_HUMAN	P78426 homo sapien
41	93.5	5.3	473	TED_HUMAN	Q75949 homo sapien
42	93.5	5.3	654	C1K4_MUSPF	Q28527 mustela put
43	93.5	5.3	1237	B3A2_MOUSE	P13808 mus musculu
44	93	5.2	580	MP12_HUMAN	P30305 homo sapien
45	93	5.2	1238	BVGS_BORBR	P26762 bordetella

ALIGNMENTS

RESULT 1	ID	TNPL_HUMAN	STANDARD	PRT	316 AA.
AC	Q13829				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor, alpha-induced protein 1, endothelial (B12 protein)				
GN	TNFAIP1 OR EDP1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Endothelial cells;				
RX	MEDLINE-92112779; PubMed-1370465;				
RA	Wolf F.W., Marks R.M., Sarma V., Byers M.G., Katz R.W., Shows T.B.,				
RA	Dixit V.M.;				
RT	"Characterization of a novel tumor necrosis factor-alpha-induced				
RT	endothelial primary response gene."				
RL	J. Biol. Chem. 267:1317-1326(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,				
RA	Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;				
RL	Submitted (Dec-2001) to the EMBL/Genbank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Lung;				
RA	Strausberg R.;				
RL	Submitted (Jan-2001) to the EMBL/Genbank/DBJ databases.				
CC	-1- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 BETA AND LIPOPOLYSACCHARIDE				
CC	(LPS).				
CC	-1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.				
CC	-----				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; M80783; AAA58385.1; -				
DR	EMBL; AY065346; AAL38649.1; -				
DR	EMBL; BC001643; AAH01643.1; -				
DR	EMBL; BC001949; AAH01949.1; -				
DR	Genew; HGNC:11894; TNFAIP1.				
DR	MIM; 191161; -				
DR	InterPro; IPR000210; BTB_POZ.				
DR	InterPro; IPR003131; K_tetra.				
DR	Pfam; PF02214; K_tetra; 1.				
DR	SMART; SM00225; BTB; 1.				
DR	PROSITE; PS50097; BTB; 1.				

[illegible]

ID	NAME	STANDARD	PRG	265 AA
Y176	HUMAN			
AC	014681;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical protein KIAA0176 (Fragment).			
GN	KIAA0176.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RI	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=96281124; PubMed=8724849;			
RA	Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIA0161-KIA0200) deduced by analysis of cDNA clones from human cell line KG-1."			
RL	DNA Ref. 3:17-24(1996).			
CC	-1 SIMILARITY: CONTAINS 1 BTF/POZ DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL: D79998; BAAL1493.1; -			
DR	InterPro: IPR000210; BTF_POZ.			
DR	InterPro: IPR003131; K_tetra.			
DR	Pfam: PF02214; K_tetra; 1.			
DR	SMART: SM00225; BTF; 1.			
DR	PROSITE: PS50097; BTF; FALSE_NEG.			
DR	Hypothetical protein.			
FT	NON_TER 1			
FT	DOMAIN 74 174 BTF			
FT	SEQUENCE 265 AA; 28801 MW; 5C7455CBBE8924 CRC64;			
QY	Query Match	8.5%; Score 151; DB 1; Length 265;		
QY	Best Local Similarity	25.0%; Pred. No. 0.0005;		
QY	Matches 73; Conservative	26; Mismatches 95; Indels 98; Gaps 14;		
DB	6 LRLGLFANOGGTSASASGRRSGQAPAGREVGEGATLPPAHCLSP-PSGQPAAGR 84			
DB	LQLDPAAMGLGSG-----GGSGVGDDGCP-----VRC-----PP-----SPRAGGTPRGH 46			
QY	85 VMFGAARARAGMYVTGEGPDSRRDDGMSSDAEDDLEPATPATATGAGHALLPDEF 144			

Db	47	GRPA	-----	VAQRLEPC	-----	PGPERRAGGGA	-----	72					
Qy	145	PEVVP	PLNIGCAHPTT	RUSTLR	-----	CYEDT	MLAMFSGRHY	1PTDSEGRYID	193				
Db	73	ARWV	LMGTYFTWTR	QTLREPK	FLCRLCCQ	DEBELDS	-----	DKDETGA	VLID	144			
Qy	194	RDGTH	EGVLMFLASG	DLPPRERY	--	RAYV	EAOYVIA	IGLTLE	ENMOPLK	ENVAQAF	251		
Db	125	BDPFF	EGGILN	LYLR	RKGLIT	YKELAE	BEVYLE	EAEFY	NIASIVR	-----	LYKERIR	174	
Qy	252	LGIM	PPYKDH	LER	-----	IYEI	ARLRAV	ORARAK	AKLSL	PSWLM	SVLTKM	298	
Db	175	-----	DNENR	ISQGV	KAVY	RYVL	QCQEE	ELTQ	WV	STYSD	GKAK	FQQLIST	218

ID	MYCN_MARMO	STANDARD:	PRT:	460 AA.
AC	061976;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DE	15-DEC-1998 (Rel. 37, Last annotation update)			
GN	N-myc proto-oncogene protein (N-mycl).			
OS	MYCN OR NMTC OR NMCT1.			
OC	Marmota monax (Woodchuck).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Marmota.			
NCBI_TxID=9995;				
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Liver;			
RC	MEDLINE=90370481; PubMed=2395655;			
RX	Fourel G., Tiollais P., Buendia M.-A.;			
RA	Nucleotide sequence of the woodchuck N-myc gene (NM-mycl).";			
RL	Nucleic Acids Res. 18:4918-4918(1990).			
CC	-1-SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER			
CC	BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.			
CC	-1-SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF			
CC	TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb-sdb.ch).			
CC	-----			
DR	EMBL; X53673; CAA37712.1; +			
DR	EMBL; X53674; CAA37712.1; JOINED.			
DR	HSSP; P25912; IHLO.			
DR	TRANSFAC; T03440; "			
DR	InterPro; IPR001092; HLH_basic.			
DR	InterPro; IPR002418; TF_Myc.			
DR	Pfam; PF00010; HLH; 1.			
DR	Pfam; PF01056; Myc_N_term; 1.			
DR	PRINTS; PR00044; LIEZIPPBMYC.			
DR	SMART; SM00353; HLH; 1.			
DR	PROSITE; PS00038; HLH_1; 1.			
DR	PROSITE; PS50888; HLH_2; 1.			
KW	Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.			
FT	DNA_BIND 258 274 ASP/GLU-RICH (ACIDIC).			
FT	DNA_BIND 377 390 BASIC DOMAIN.			
FT	DNA_BIND 391 430 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).			
FT	DNA_BIND 429 450 LEUCINE-ZIPPER (POTENTIAL).			
FT	MOD_RES 257 257. PHOSPHORYLATION (BY CK2)			
FT	MOD_RES 257 257. (BY SIMILARITY).			
FT	MOD_RES 259 259 PHOSPHORYLATION (BY CK2)			
FT	MOD_RES 259 259. (BY SIMILARITY).			
SEQ	SEQUENCE 460 AA; 49192 MW; 8A1666C62F5B02E CXC64;			

Query Match 6.9%; Score 123; DB 1; Length 460;

Best Local Similarity 19.9%; Pred. No. 0.097;
Matches 69; Conservative 48; Mismatches 115; Indels 114; Gaps 14;

QY 4 ATLRNKGKGRRLRRRLPALRLGELPANOGCTSAASASRRSGQAPGRERVGEG 63
DB 130 ANSEKQHRGRP-----PAAQPA-----TPGAAANRAGHGCTAGRGAALPA 176
QY 64 AVALPPHCLSP-----PSGAPAAHVMGGAARRARGMV-----VT 100
DB 177 ELAHPAAECVDPAVVPFVNKDPAPVPAPAGSAPVGAAGAAPASAAVAAPRLG 236
QY 101 GKEPD-----SRKDDGAMSSSDAEDPLEP-----ATPTAQGHALPL 140
DB 237 GRPANGGDHAKALSTSEDLTSDDEDEDEDEEDVTYVERKRRSSSKAVTFTTIT 296
QY 141 PDEPPVPLNIGAFHTTRLSTRCYEDTMLAMFSGRHYPDSGREYIDRGTHTFG 200
DB 297 VR--FKNALGIGRAO--SEELIKRC-----VPHOHNAAAPSP----- 333
QY 201 DVALNFLRSGDLPPRRERAVYKRAOYTAIGPLLEOLENMOPLGK----- 246
DB 334 -----YVESDAPQKIKSVSPRLKSVIP--PKAKSLSPNDSHDSERRRHNLIER 387
QY 247 -----VRQAFGLMPYKDKHLEIVEIARAVQKARFKLSLT 287
DB 388 ORANDLRSSFLT-----RDHVPFLVK-----NEKAKVILKKVAT 423

RESULT 4
ID CIK5_MUSPF STANDARD; PRT; 601 AA.
AC P79197;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.5.
GN KCNA5.
OS Muscivora putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Muscivora.
OX NCBI_TaxID=9669;
[1]
RP SEQUENCE FROM N.A.
RC Tissue-Heart atrium;
RA Schlegel T., Folander K., Swanson R.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U45979; AAB41145.1; -

DR HSP, Q54397.1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+-channel_pore.
DR InterPro: IPR004052; KV15channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+-channel_nlg.
DR InterPro: IPR003972; Shaker_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01512; KV15CHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01496; SHAKERCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 240 258
FT TRANSMEM 314 334
FT TRANSMEM 345 366
FT TRANSMEM 386 407
FT TRANSMEM 422 443
FT TRANSMEM 483 504
FT DOMAIN 370 375
FT CARBOHYD 114 114
FT CARBOHYD 179 179
FT CARBOHYD 288 288
SQ SEQUENCE 601 AA; 65889 MW; 142DB9B8CB43FE0 CRC64;

Query Match 6.9%; Score 122.5; DB 1; Length 601;
Best Local Similarity 23.8%; Pred. No. 0.15;
Matches 81; Conservative 39; Mismatches 148; Indels 73; Gaps 17;

QY 26 LRLGELPANOGCTSAASASRRSGQAPGRERVGATALPAPCLSPSGQAPAGRY 85
DB 1 MEIALVPLENG-----AMTVRGGEAGYGCSSQ--ALGELQCPAGLSGPREPAP-- 51
QY 86 MGAARARGMVYVGRPDSRRDAMSSDAEDPLEP--APPTAQGHALPLPQEF 144
DB 52 -----RARG-----TORGVD-----PGRPPLPPLPDPQPRRLPPEDEBEGPALGMAE 97
QY 145 PEV-----VPLNIGAHFTTRLSTRCYEDTMLAMFSG--RHYPDSGREYFD 193
DB 98 DQVLGAGSLHQVRLINISGLRFTQGLAQPNLLGDPARLRARFQPLRNE--YFFD 155
QY 194 RGTGRGDTANLRSGD---LPPREVRAYVKAQYTAIG-PLLEQL-----ENMQP 241
DB 156 RRPSPFDGLYYOOSGRRLRPVNSLDVFADEIRYQLDEAMERREDEGFIKEEKP 215
QY 242 L-KGEVRQAFGLMPYKDKHLEIVEIARAVQKARFARKLSLTPSWLMVLIKMP 300
DB 216 LPRNEFQRYVYL-----IIEYSSSANGAIALVSVLIISITTCLETLPE 263
QY 301 GVTSWINARRLYLEPI-----GPERONNEKSPVQLPAG 336
DB 264 -----FRDERELLRHPVPVHPQLGSPRGAN--GSGPLAPP 298

RESULT 5
ID CIKL_DROME STANDARD; PRT; 490 AA.
AC P17971; Q9YV11;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Shal (Shal2).
GN SHAL OR SHAL2 OR CG9262.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90239553; PubMed-2333511;
 RA Wel A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K⁺ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse."
 RL Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90245688; PubMed-2336395;
 RA Wel A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila."
 RL Nucleic Acids Res. 18:2173-2174(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Berkeley;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blake J.R., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck Y., Brokstein P., Brotter P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jostali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel P.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Moulton G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson K.D., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -1- SUBUNIT: HETEROTRIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL: M32660; AAA28895.1; -
 DR EMBL: AE003516; AAF69144.1; ALT_SEQ.
 DR PIR: A35312; A35312.
 DR PIR: S12747; S12747.
 DR Flybase: FBgn0005564; Shal.
 DR InterPro: IPR000210; B7B_POZ.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003091; K-channel.
 DR InterPro: IPR003131; K-tetra.
 DR InterPro: IPR003968; K-channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003975; Shal_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1491; KYCHANNEL.
 DR PRINTS: PRO1497; SHALCHANNEL.
 DR SMART: SM00225; B7B_1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Alternative splicing.
 FT TRANSMEM 186 204 SEGMENT S1.
 FT TRANSMEM 229 250 SEGMENT S2.
 FT TRANSMEM 261 282 SEGMENT S3.
 FT TRANSMEM 290 308 SEGMENT S4.
 FT TRANSMEM 324 345 SEGMENT S5.
 FT TRANSMEM 385 406 SEGMENT S6.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 490 AA; 55918 MW; E178ELC89B07DA74 CRC64;
 Query Match 6.8%; Score 121; DB 1; Length 490;
 Best Local Similarity 27.0%; Pred. No. 0.15;
 Matches 41; Conservative 17; Mismatches 48; Indels 46; Gaps 6;
 QY 128 PTAQAGALPLPLPEP-----EYPLNIGAHFTTRSLRCYDYMILAMFSOR 179
 DB 20 PIATH-----PLPPPMKRRRTDKLLINVSQRRETWNTLEKYDITLGS--NR 72
 QY 180 HYIPDSGRFIDGTHGFVNLFLSGDLP-PRERVAVYKEAQYVAIPLEQLN 238
 DB 73 EFDDECKEFPDNDPLFRILINYYRKGKLRHCELTSTDE----- 117
 QY 239 MQLPKERVAFLGLMP-----YKDKHLR 264
 DB 118 -----ELAFGLMDVLDICCYEDYRDR 140
 RESULT 6
 CIRC_MOUSE
 ID CIRC_MOUSE STANDARD; PRT; 602 AA.
 AC 061762;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.5 (Kv1.5).
 GN KCNA5.
 OS Mus musculus (Mouse).

RP SEQUENCE FROM N.A.
 RC TISSUE-Heart:
 RX MEDLINE-92241872; PubMed-1349297;
 RA Curran M.E., Landes G.M., Keating M.T.;
 RT "Molecular cloning, characterization, and genomic localization of a
 human potassium channel gene.";
 RL Genomics 12:729-737(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN REGULATING THE SECRETION OF INSULIN
 IN NORMAL PANCREATIC ISLETS.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PANCREATIC ISLETS AND INSULINOMA.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M60451; AAA61276.1; -
 DR EMBL: M55513; AAA36422.1; -
 DR EMBL: M83254; AAA60146.1; -
 DR PIR: B39922; B39922.
 DR HSSP: O54397; 1BL8.
 DR Genew: HGNC:6224; KCNA5.
 DR MIM: 176267; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004052; KV15channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01512; KV15CHANNEL.
 DR PRINTS: PR01491; KVCCHANNEL.
 DR PRINTS: PR01496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation; Repeat.
 RT DOMAIN
 FT 61 82
 FT REPEAT
 FT 61 71
 FT REPEAT
 FT 72 82
 FT TRANSMEM
 FT 251 269
 FT TRANSMEM
 FT 325 345
 FT TRANSMEM
 FT 356 377
 FT TRANSMEM
 FT 398 419
 FT TRANSMEM
 FT 434 455
 FT TRANSMEM
 FT 495 516
 FT DOMAIN
 FT 94 99
 FT DOMAIN
 FT 382 387
 FT CARBOHYD
 FT 125 125
 FT CARBOHYD
 FT 190 190

FT MOD RES 557 557
 FT CONFLICT 55 55
 FT CONFLICT 138 138
 FT CONFLICT 154 154
 FT CONFLICT 187 188
 FT CONFLICT 214 214
 FT CONFLICT 228 228
 FT CONFLICT 282 282
 FT CONFLICT 307 307
 FT CONFLICT 579 613
 SO SEQUENCE 613 AA; 67168 MW; 6324F704F127C5BC CMC64;
 Query Match 6.78; Score 119.5; DB 1; Length 613;
 Best Local Similarity 22.5%; Pred. No. 0.24;
 Matches 62; Conservative 27; Mismatches 101; Indels 85; Gaps 11;
 OY 26 LRLEPLPNOGTSASASGRRSGAAGRVERVEATLAPAHCLSPSGQRA-AGR 84
 DB 1 MEIALVPLENGAMTVRGDENRACGQA-----TGELQCPYAGLSDGPKRAPKGR 54
 OY 85 VMPGAARRAGMYVTGREDPSRRQDGAMSSSDAEDDELPATATONGHALPLPOFE 144
 DB 55 -GAQDA-----DSGYRPLPLPDGVRPLPLPEL 85
 OY 145 P-----EYVPLNIGAHFTTRLSLRCEYDTM 171
 DB 86 PRPRRPPEDEBERDDELGTVEDQALGTASLHGRVHINIGLPERQGLAQFPNTL 145
 OY 172 LAAMFSGRHY-PRDSERYFLDRGTHFGDYANLRSGD--LPPREVRVAYEAOY 227
 DB 146 LGDPARKLPYDPPLNNE--YFDRNRPSFDGLTYTQSGRLRRVNVSLDFAEIRRY 203
 OY 228 AIG-PLLEQL-----ENMQPL-KGEKVRQAF 252
 DB 204 QLGDEMERFREDGEFTKEERKPLPRNFQROVWL 238
 RESULT 8
 CIRS_RAT
 ID CIRS_RAT STANDARD; PRT: 602 AA.
 AC P19024;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.5 (Kv1) (RCK7).
 GN KCNA5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-90297965; PubMed-2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Foldander K., Lunteau C.J., Antanavage J., Oliva C., Bulhrov S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SMRT/TRAC-2 (SHOWN HERE) AND
 CC TRAC-1; ARE PRODUCED BY ALTERNATIVE SPLICING. TRAC-1 CONTAINS ONLY
 CC THE C-TERMINAL RECEPTOR-INTERACTING DOMAIN AND ACTS AS AN
 CC ANTI-REPRESSOR.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION ARE
 CC DETECTED IN LUNG, SPLEEN AND BRAIN.
 CC -1- INDUCTION: REGULATED DURING CELL CYCLE PROGRESSION.
 CC -1- DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
 CC ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
 CC AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
 CC INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
 CC DOMAINS (ID1 AND ID2).
 CC -1- DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
 CC SEQUENCE REFERRED TO AS THE CORN BOX. THIS MOTIF IS REQUIRED AND
 CC SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES
 CC FLANKING THE CORN BOX DETERMINE NUCLEAR HORMONE RECEPTOR
 CC SPECIFICITY.
 CC -1- SIMILARITY: CONTAINS 1 SANT-A DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF113003; AAD20946.1; -
 CC EMBL; AF125672; AAD22973.1; -
 CC EMBL; U37146; AAC50236.1; -
 CC EMBL; S83390; AAB50847.1; -
 CC EMBL; U80750; AAB91446.1; -
 CC TRANSFAC; T04689; -
 CC Gene; HGNC:7673; NCOR2.
 CC MIM; 600848; -
 CC InterPro: IPR001005; MYB_DNA_binding.
 CC Pfam; PF00249; myb_DNA-binding; 2.
 CC SMART; SM00395; SANT; 2.
 CC PROSITE; PS50090; MYB_3; 1.
 CC Nuclear protein; Transcription regulation; DNA-binding; Repressor;
 CC Colled coil; Alternative splicing.
 CC -----
 CC FT DOMAIN 174 215 COILED COIL (POTENTIAL).
 CC FT DOMAIN 254 312 INTERACTION WITH SIN3A/B (BY SIMILARITY).
 CC FT DNA_BIND 429 474 SANT-A (POTENTIAL).
 CC FT MYB 613 657 MYB.
 CC FT PRO-RICH 522 561 PRO-RICH.
 CC FT CORN_BOX_OF_ID1 2342 2346 CORN BOX OF ID1.
 CC FT POLY-GLN 494 510 POLY-GLN.
 CC FT POLY-LYS 682 685 POLY-LYS.
 CC FT POLY-PRO 994 1002 POLY-PRO.
 CC FT POLY-GLY 1384 1389 POLY-GLY.
 CC FT POLY-PRO 1842 1846 POLY-PRO.
 CC FT POLY-PRO 2479 2482 POLY-PRO.
 CC FT MISSING (IN ISOFORM TRAC-1).
 CC FT MISSING (IN ISOFORM TRAC-1).
 CC FT L -> P (IN REF. 2).
 CC FT K -> E (IN REF. 2).
 CC FT L -> W (IN REF. 2).
 CC FT MISSING (IN REF. 2).
 CC FT A -> P (IN REF. 2).
 CC FT SS -> EF (IN REF. 5).
 CC FT S -> T (IN REF. 2).
 CC FT MISSING (IN REF. 2).
 CC FT BTRAPREP -> PEDIPAPES (IN REF. 2).
 CC FT G -> L (IN REF. 2).
 CC FT S -> F (IN REF. 2).
 CC FT CONFLICT 814 814

FT CONFLICT 817 817 A -> S (IN REF. 2).
 FT CONFLICT 889 889 G -> R (IN REF. 2).
 FT CONFLICT 1023 1030 SRSPAPPA -> MEAMDAHP (IN REF. 3).
 FT CONFLICT 1034 1034 A -> AEKPYFPA (IN REF. 2).
 FT CONFLICT 1894 1894 K -> T (IN REF. 4).
 FT CONFLICT 2494 2494 P -> A (IN REF. 4).
 SQ SEQUENCE 2517 AA; 274031 MW; F5805C01761258C0 CRC64;
 Query Match 6.3%; Score 112; DB 1; Length 2517;
 Best local similarity 21.9%; Pred. No. 4.6;
 Matches 68; Conservative 23; Mismatches 104; Indels 116; Gaps 12;
 QY 15 PLRRRLPALPALRG-ELPANOGTSAASSGRRSGCAPARRVGEATAPALPACLT 73
 DB 1440 PLAPRLKESSTIGTGKDYTGASTGSKKHVRS-----LIGSGRT-PPVHPL 1490
 QY 74 SPSPGPAAGRV-----MPGAARARAGNV----- 98
 DB 1491 DVADARALRACYESLSKSPGTASSGSIAGAPVYELKPRQSPPLYEDHGAFF 1550
 QY 99 -----VTGREPDSRRDQGANSSSDAEDDFLEPAP-----TATQAGHALPLP 141
 DB 1551 AGHLPRGSPYTMKPTPTRLQSGSLSSSKASQDRKLTSPRIAKSPHSTVEHHHPISP 1610
 QY 142 QE-----PEVYVNLIGAHFTTRLSL-----L 164
 DB 1611 YEHLLRGVSGVDLYRSHIPLAFDPTISPRGIFLDAAYVPLRHAPNPTYPHYLYLI 1670
 QY 165 RCVEDTMLAMFSGRHIIPTDSEGRYFIDRGTHFGVDLNLBSGD-----LPPRRVNAV 220
 DB 1671 RGPVDT---AALENKQTLIND-----YITSCQMHNTATANAORADMLRGLSPRESSIAL 1722
 QY 221 YKEAOYVYAGP 231
 DB 1723 -----NYAAGP 1728
 RESULT 10
 CITS_RABIT STANDARD; PRT; 598 AA.
 AC P50638;
 NC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.5.
 GN KCNA5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Heart;
 RX MEDLINE=96032538; PubMed=755635;
 RA Sasaki Y., Ishii K., Nunoki K., Yamagishi T., Taira N.,
 RT "The voltage-dependent K⁺ channel (Kv1.5) cloned from rabbit heart
 RT and facilitation of inactivation of the delayed rectifier current by
 RT the rat beta subunit".
 RL FEBS Lett. 372:20-24(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Portal vein;
 RA Clement-Chomienne O., Ishii K., Walsh M.P., Cole W.C.;
 RT "Rabbit portal vein Kv1.5".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Smooth muscle;
 RA Tate R.J., Osipenko O.N., Kempall F.E.J., Gurney A.M.;
 RT "Identification of a voltage-gated potassium channel (Kv1.5) in rabbit
 RT pulmonary artery smooth muscle".
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM

DR EMBL: X16001; CAA34132.1; -
 DR EMBL: M30312; AAA42035.1; -
 DR EMBL: M31744; AAA41500.1; -
 DR PIR: S06708; S06708.
 DR PIR: JH0168; JH0168.
 DR HSRP: Q54397; 1BL8.
 DR InterPro: IPR000210; BTR_POR.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004050; KV13channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_channel.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PR0169; K3CHANNEL.
 DR PRINTS: PR01510; KV13CHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 185 203 SEGMENT S1.
 FT TRANSMEM 245 266 SEGMENT S2.
 FT TRANSMEM 278 298 SEGMENT S3.
 FT TRANSMEM 313 331 SEGMENT S4.
 FT TRANSMEM 348 367 SEGMENT S5.
 FT TRANSMEM 409 431 SEGMENT S6.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 470 470 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CONFLICT 106 106 F -> L (IN REF. 1).
 FT CONFLICT 181 181 G -> R (IN REF. 3).
 FT CONFLICT 430 430 V -> L (IN REF. 3).
 SQ SEQUENCE 525 AA; 58424 MW; 6DA869D5471C401 CRC64;
 Query Match 6.0%; Score 106.5; DB 1; Length 525;
 Best Local Similarity 27.0%; Pred. No. 1.7;
 Matches 50; Conservative 24; Mismatches 72; Indels 39; Gaps 10;
 OY 65 PALPACSPSPGPGAGRVMGCAARAGVAVVVGREPDSDRSGDSSDADEFELE 124
 DB 2 TVVPGDHLLEP-----EAGG-----GGGDP--GGGCVSGGC--DYE 37
 OY 125 PATPATATGHALPLLPQE-FPEVPLNIGAHFTTRILTKCYEDTMA-AMFSGHYI 182
 DB 38 PLPPALPAGE-----GQCCGERVYINISGLRFEIQLKCEPEHLLGDPKRMATFD 91
 OY 183 PIDSSEGRITDRDGHFGDVLNLRSGD--LPPREVRVAVYEAQYVYAGPLLEQLENN 239
 DB 92 PLRNE--YFEDRRRPSFDAILVYVYGGGRIRRVVNPIDIFSEIRRYQLGE--EAMEKF 147
 OY 240 OPLKG 244
 DB 148 REDEG 152
 RESULT 12
 CIRS DROME STRAND: PRT: 656 AA.
 AC P08B10; P08511; Q24521; P08512; P08513; Q24277; Q9VWZ9;
 DT 01-AUG-1988 (Rel. 08; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Voltage-gated potassium channel protein Shaker.
 GN SH OR CG12348.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;

RN [1]
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
 RX MEDLINE=87292096; PubMed=2441471;
 RA Tempel B.L., Papazian D.M., Schwarz T.L., Jan Y.N., Jan L.Y.;
 RT "Sequence of a probable potassium channel component encoded at Shaker
 locus of Drosophila."
 RL Science 237:770-775(1987).
 RN [2]
 RP SEQUENCE OF 1-257 FROM N.A. (BETA ISOFORM).
 RX MEDLINE=87273502; PubMed=2440582;
 RA Kamb A., Iverson L.E., Tanouye M.A.;
 RT "Molecular characterization of Shaker, a Drosophila gene that encodes
 a potassium channel."
 RL Cell 50:405-413(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (DELTA ISOFORM).
 RC STRAIN-Canton-S, and Oregon-R;
 RA Baumann A., Krah-jentgens I., Mueller R., Mueller-Holtkamp F.,
 RA Seidel R., Keschemethy N., Casel J., Ferrus A., Pongs O.;
 RT "Molecular organization of the maternal effect region of the Shaker
 complex of Drosophila: characterization of an I(A) channel transcript
 with homology to vertebrate Na(+) channel."
 RL EMBO J. 6:3419-3429(1987).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA, BETA, DELTA, GAMMA AND EPSILON).
 RC STRAIN-Canton-S;
 RX MEDLINE=86296413; PubMed=2456921;
 RA Pongs O., Keschemethy N., Mueller R., Krah-jentgens I.,
 RA Baumann A., Kiltz H.H., Canal I., Llamazares S., Ferrus A.;
 RT "Shaker encodes a family of putative potassium channel proteins in
 the nervous system of Drosophila."
 RL EMBO J. 7:1087-1096(1988).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA, BETA, GAMMA AND B).
 RX MEDLINE=88122563; PubMed=2448635;
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
 RT "Multiple potassium-channel components are produced by alternative
 splicing at the Shaker locus in Drosophila."
 RL Nature 331:117-142(1988).
 RN [6]
 RP ERRATUM.
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
 RL Nature 332:740-740(1988).
 RN [7]
 RP SEQUENCE OF 450-534 FROM N.A.
 RC STRAIN-H4;
 RX MEDLINE=90166523; PubMed=3272175;
 RA Kamb A., Tseng-Crank J., Tanouye M.A.;
 RT "Multiple products of the Drosophila Shaker gene may contribute to
 potassium channel diversity."
 RL Neuron 1:421-430(1988).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Bendale J., Beyers R., Bhatnagar S.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandal D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Dwyer A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Galbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=66149381; PubMed=2869488;
 RA Stanton L.W., Schwab M., Bishop J.M.;
 RT "Nucleotide sequence of the human N-myc gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1772-1776(1986).
 RP SEQUENCE FROM N.A.
 [1]
 RX MEDLINE=86092232; PubMed=3510398;
 RA Kohl N.E., Iegouy E., Depinho R.A., Nisen P.D., Smith R.K.,
 RA Gee C.E., Alt F.W.;
 RT "Human N-myc is closely related in organization and nucleotide
 RT sequence to c-myc.";
 RL Nature 319:73-77(1986).
 RP SEQUENCE FROM N.A.
 [3]
 RX MEDLINE=88202932; PubMed=2834684;
 RA Ison J.M., Rabbits P.H.;
 RT "Sequence of a germ-line N-myc gene and amplification as a mechanism
 RT of activation.";
 RL Oncogene 2:399-402(1985).
 RP SEQUENCE OF 71-464 FROM N.A.
 [4]
 RX MEDLINE=86179901; PubMed=3008339;
 RA Slamon D.J., Boone T.C., Seeger R.C., Keith D.E., Chazin V., Lee H.C.,
 RA Souza L.M.;
 RT "Identification and characterization of the protein encoded by the
 RT human N-myc oncogene.";
 RL Science 232:768-772(1986).
 RP SEQUENCE OF 313-464 FROM N.A.
 [5]
 RX MEDLINE=85215633; PubMed=2987858;
 RA Nischtsch R.W., Melera P.W.;
 RT "Nucleotide sequence of the 3' exon of the human N-myc gene.";
 RL Nucleic Acids Res. 13:2545-2558(1985).
 RP PHOSPHORYLATION BY CK2.
 RX MEDLINE=93049352; PubMed=1425701;
 RA Hagihara T., Nakaya K., Nakamura Y., Nakajima H., Nishimura S.,
 RA Taya Y.;
 RT "Specific phosphorylation of the acidic central region of the N-myc
 RT protein by casein kinase II.";
 RL Eur. J. Biochem. 209:945-950(1992).
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING FETAL DEVELOPMENT.
 CC -1- DISEASE: AMPLIFICATION OF THE N-MYC GENE IS ASSOCIATED WITH A
 CC VARIETY OF HUMAN TUMORS, MOST FREQUENTLY NEUROBLASTOMA, WHERE THE
 CC LEVEL OF AMPLIFICATION APPEARS TO INCREASE AS THE TUMOR
 CC PROGRESSES.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/genes/NMYC112.html".
 CC -----
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 CC -----
 CC EMBL: X03294; CAA27037.1; -;
 CC EMBL: X03295; CAA27038.1; -;
 CC EMBL: M13241; AAA36371.1; ALT_INIT.
 CC EMBL: M13228; AAA36370.1; -;

DR EMBL: X02363; -; NOT_ANNOTATED_CDS.
 DR EMBL: Y00664; CAA68678.1; ALT_INIT.
 DR PIR: A25744; TVHUM2.
 DR PIR: A01355; TVHUMC.
 DR PIR: A22937; A22937.
 DR PIR: S02249; S02249.
 DR HSR: P25912; HLLO.
 DR TRANSFAC: T02379; -;
 DR Genew: HGNC:7559; MYCN.
 DR MIM: 164840; -;
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR002418; TF_MYC.
 DR Pfam: PF01056; HLH_1.
 DR Pfam: PF01056; MYC_N-term; 1.
 DR PRINTS: PR00044; LEUZIPPRMYC.
 DR SMART: SM00353; HLH; 1.
 DR PROSITE: PS00038; HLH_1; 1.
 DR PROSITE: PS50888; HLH_2; 1.
 KW Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.
 FT DOMAIN 262 278
 FT DNA_BIND 381 394
 FT DOMAIN 395 434
 FT DOMAIN 433 454
 FT MOD_RES 261 261
 FT MOD_RES 263 263
 FT MOD_RES 227 227
 FT CONFLICT 363 363
 FT CONFLICT 363 363
 SQ SEQUENCE 464 AA; 49561 MW; 560E885602E30DAD CRC64;

Query Match 5.9%; Score 105.5; DB 1; Length 464;
 Best Local Similarity 19.4%; Pred. No. 1.7;
 Matches 71; Conservative 43; Mismatches 125; Indels 127; Gaps 14;

QY 11 GKGPLRRRLPLAL-----PALRLGELPANOG-----GTSASASS 45
 DB 100 GGLGGLPNPVIILDDCMGSEFSAEKLERAYSEKQHRGPGPTAGSTASPGASAPAG 159
 QY 46 GRNSGAPAGHERVVEGATALLPPAHCLSP-----PSGAPAG-RV 85
 DB 160 RGHGAGAGAGAGALPAELHAPAECDPAVFPVKNKEPAPVAPAPAPAGAPAV 219
 QY 86 MFGARARA-RGMVYVTGEPDSRRDGS-----ANSSAEDFLEPAFPTATQ 132
 DB 220 ASGAGIAAP 271
 QY 133 AGHALPLPQEPFVVPVNICGAFETRLSTLRCYEDTML--AAFGSR-----H 180
 DB 272 -----DEEEDIDVYTVKRRSSSWTKAVTTITIVRRKNALGFGRAOSSLEIKR 322
 QY 181 YIPFDSGRFTIDRGHFGVNLFLNSGDLPPRRERVAAYKQVYVIGPLEQLENNQ 240
 DB 323 CLPFOOHNVYAAPSP-----YVESEDAPQPKIKSEASPRDLKSVIP--PRAKLS 371
 QY 241 PLNKEK-----VRAFLGIMFYVDHERLYEIALRVQKARARA 281
 DB 372 PRNSDSEDSERRRNHILRORRNDLRSSFTLV---RDHVELVK-----NEAAKRV 421
 QY 282 KIKSLT 287
 DB 422 ILKRAIT 427
 RESULT 14
 5E5_RAT ID 5E5_RAT STANDARD; PRT; 925 AA.
 AC 063003;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 5E5 antigen.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OM protein - protein search, using SW model

Run on: February 12, 2003, 11:07:36 ; Search time 13 seconds

(Without alignments)
674.097 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780
Sequence: 1 MVTAVLRNRKRGKPLRRP.....NNEKSPVQLPAGVFOHEMG 343Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCF_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	560.5	31.5	120	US-10-024-579-5	Sequence 5, Appl1
2	314.5	17.7	106	US-10-024-579-7	Sequence 7, Appl1
3	305	17.1	56	US-09-864-761-14673	Sequence 34673, A
4	245	13.8	175	US-09-925-299-879	Sequence 879, App
5	174.5	9.8	238	US-10-024-579-16	Sequence 16, Appl
6	174.5	9.8	257	US-10-024-579-14	Sequence 14, Appl
7	174.5	9.8	264	US-10-024-579-12	Sequence 12, Appl
8	174.5	9.8	283	US-10-024-579-10	Sequence 10, Appl
9	157	8.8	378	US-09-764-864-1240	Sequence 1240, Ap
10	140.5	7.9	213	US-10-024-579-2	Sequence 2, Appl1
11	127	7.1	636	US-10-062-879-2	Sequence 4, Appl1
12	127	7.1	655	US-10-062-879-2	Sequence 2, Appl1
13	120.5	6.8	532	US-09-993-811-6	Sequence 6, Appl1
14	113.5	6.4	418	US-09-946-807-3	Sequence 3, Appl1
15	113.5	6.4	418	US-09-795-686-3	Sequence 3, Appl1
16	113.5	6.4	418	US-09-795-686-3	Sequence 3, Appl1
17	112	6.3	2507	US-09-819-104A-2	Sequence 2, Appl1
18	111	6.2	1907	US-09-833-292-39	Sequence 39, Appl
19	109	6.1	286	US-09-737-149-39	Sequence 39, Appl

20	108	6.1	351	10	US-09-350-874-61	Sequence 61, Appl
21	105.5	5.9	224	9	US-09-738-626-6616	Sequence 6616, Ap
22	104.5	5.9	447	9	US-09-975-719-351	Sequence 351, App
23	102	5.7	275	10	US-09-737-149-10	Sequence 10, Appl
24	101.5	5.7	261	9	US-09-843-676-174	Sequence 174, App
25	101.5	5.7	261	9	US-09-438-186-174	Sequence 174, App
26	101	5.7	399	10	US-09-893-737-10	Sequence 10, Appl
27	100.5	5.6	527	9	US-09-854-133-216	Sequence 216, App
28	100.5	5.6	527	10	US-09-738-973-216	Sequence 943, App
29	100	5.5	580	10	US-09-925-301-943	Sequence 2, Appl1
30	98.5	5.5	874	10	US-09-950-370-12	Sequence 12, Appl
31	98.5	5.5	902	10	US-09-854-133-434	Sequence 434, App
32	98	5.5	687	9	US-09-764-868-661	Sequence 434, App
33	97	5.4	456	9	US-09-989-920-175	Sequence 175, App
34	97	5.4	456	10	US-09-993-811-12	Sequence 2, Appl1
35	97	5.4	456	10	US-09-974-712-2	Sequence 12, Appl
36	96.5	5.4	454	10	US-09-953-811-12	Sequence 434, App
37	96.5	5.4	1702	9	US-09-738-973-434	Sequence 434, App
38	96.5	5.4	7968	9	US-10-077-130-5	Sequence 5, Appl1
39	94.5	5.3	332	9	US-09-764-868-1013	Sequence 1013, Ap
40	93.5	5.2	566	9	US-09-797-500-2	Sequence 2, Appl1
41	93	5.2	365	9	US-10-108-605-343	Sequence 343, App
42	92.5	5.2	739	9	US-09-974-298-159	Sequence 159, App
43	92.5	5.2	739	9	US-10-028-072-178	Sequence 478, App
44	92.5	5.2	739	9	US-10-121-049-478	Sequence 478, App
45	92.5	5.2	739	9	US-10-121-049-478	Sequence 478, App

ALIGNMENTS

RESULT 1
US-10-024-579-5
Sequence 5, Application US/10024579
Patent No. US20020119522A1
GENERAL INFORMATION:
APPLICANT: Fridde, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024, 579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258, 595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 120
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-5

Query Match 31.5%; Score 560.5; DB 12; Length 120;
Best Local Similarity 91.7%; Pred. No. 3.5e-40;
Matches 110; Conservative 3; Mismatches 2; Indels 5; Gaps 2;

DB 156 MVTAVLRNRKRGKPLRRP.....NNEKSPVQLPAGVFOHEMG 343
61 HFTRLSLRKYEDTLMAMFSGRRHYIPTDSEGRYFIDRGTGTFGVSPSTINFTVLAAD 120

RESULT 2
US-10-024-579-7
Sequence 7, Application US/10024579
Patent No. US20020119522A1
GENERAL INFORMATION:

APPLICANT: Friddie, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522a1el Human Ion Channel-Related Proteins
FILE REFERENCE: Lex-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 106
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-7

Query Match 17.7%; Score 314.5; DB 12; Length 106;
Best Local Similarity 83.6%; Pred. No. 1.2e-19;
Matches 61; Conservative 5; Mismatches 2; Indels 5; Gaps 2;

QY 143 EPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYFDIDGTHFQV 202
DB 34 QPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYFDIDGTHFQV 93

QY 203 ----LNF-LNSGD 210
DB 94 SPTINTVVLACD 106

RESULT 3
US-09-864-761-34673
Sequence 34673, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Neomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34673
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006001.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 4.6
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL - 12
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 5.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 4.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL - 14
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL - 8.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 5.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 6.4
OTHER INFORMATION: EST_HUMAN HIT: A1674184.1, EVALUATE 4.00e-28
OTHER INFORMATION: SWISSPROT HIT: Q13829, EVALUATE 9.00e-07

US-09-864-761-34673

Query Match 17.1%; Score 305; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 EPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYFDIDGTHF 199
DB 1 EPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYFDIDGTHF 56

RESULT 4
US-09-925-299-879
Sequence 879, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 879
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (168)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-299-879

Query Match 13.8%; Score 245; DB 10; Length 175;
Best Local Similarity 37.5%; Pred. No. 1.6e-13;
Matches 63; Conservative 26; Mismatches 63; Indels 16; Gaps 3;

QY 108 ROGAMSSDAEDDFLPATPTAQAALPLQLQEPPEVPLNIGAHFTTSLTLCY 167
DB 12 RPVGKMTSQTPLPSPRRRPTMS-----TVELNNGEPRHTTGLTKRK 57

```

OY      168 EDMLAAEFSRHHYPTDSESRGHTDRGCTHFGVLTNFRSGDDLPERRRYAVYKKAQXY 227
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          |:::|||||:::|||||:::|||||:::|||||:::|||||
Db       58 PGSLAEFFSSLAASADSAERGFIDRPSTIFRFPLDLTKGV-PIQHIEVYREAQFY 116
          ||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY      228 AIGPLEOLENMOPKGEKV-RQAFLGIAPYKDHLERIVEIARLAV 274
          ||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db       117 EIKPVLTKLEDMPOIFGEQVSRRKQLLCRAFTARFWELMVALAREAI 164
          ||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
US-10-024-579-16
; Sequence 16, Application US/10024579
; Patent No. US20020119522A1
GENERAL INFORMATION:
APPLICANT: Fridgde, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 238
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-16

Query Match           9.8%; Score 174.5; DB 12; Length 238;
Best Local Similarity 35.2%; Pred. No. 1.9e-07;
Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;

OY      125 PATPATQAGNALPLLPEFPEPVYLVNTGNAFTRLSTICYEEDTMLAAMSGRHNYPT 184
          |||||
          |:::|||||:::|||||:::|||||:::|||||
Db       10 PVSPILAQQ-GIDPLPQLRKSNAEPVVIDVGHNYSLSLATNTYPDSRKSLNGTEPYTL 68
          |||||
          |:::|||||:::|||||:::|||||
OY      185 DS-EGRVFIDRDGTTHFGDVLTNFRSGDDLPERRRYA---AVYKKAQYVAIGPLEOLENMQ 240
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Db       69 DSLKHGYTIDRGSEIFRVYLSFLTRSKILLDDPDFDFSLATFEANYQLQPVRLELRNQ 128
          ||:::|||||
          |:::|

OY      241 PLKGEKVR 248
          :::|
Db       129 QEOEQRRR 136

RESULT 6
US-10-024-579-14
; Sequence 14, Application US/10024579
; Patent No. US20020119522A1
GENERAL INFORMATION:
APPLICANT: Fridgde, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 257
TYPE: PRT
ORGANISM: homo sapiens

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US-10-024-579-14	Query Match	9.8%; Score 174.5; DB 12; Length 257;	
	Best Local Similarity	35.2%; Pred. NO. 2.1e-07;	
	Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;		
OY 125 PATPATQAGNALPLLPQEFPEVYPLNTIGCANFTTRLSCTICYEEDTMAMFSGRHYYPT	184		
DB 10 PVSPLPAAQ-GIPLPQOLTKRSNAPVHIDVGHHYTSLSLATLTKYPPSRISRLNGTEPYTL	68		
OY 185 DS-BGRYVIFDRDGTAFRGVNLNFRSGDLPFRBRVR--AVYEAQYVAIGPLLEQLENWQ	240		
DB 69 DSLKHHYIFDRDGEIFRYYLSLSTRISKLLLPDDEFDSLIYEANYTOLQPVRELERWQ	128		
OY 241 PLKGEKVR 248			
DB 129 QOEQRRR 136			
RESULT 7			
US-10-024-579-12			
/ Sequence 12, Application US/10024579			
/ Patent No. US20020119522A1			
GENERAL INFORMATION:			
APPLICANT: Friddele, Carl Johan			
APPLICANT: Gerhardt, Brenda			
APPLICANT: Hilbun, Erin			
APPLICANT: Turner, C. Alexander Jr.			
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related			Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same			
FILE REFERENCE: LEX-0274-USA			
CURRENT APPLICATION NUMBER: US/10/024, 579			
CURRENT FILING DATE: 2001-12-18			
PRIOR APPLICATION NUMBER: US 60/258,595			
PRIOR FILING DATE: 2000-12-28			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 12			
LENGTH: 264			
TYPE: PRT			
ORGANISM: homo sapiens			
US-10-024-579-12			
Query Match	9.8%; Score 174.5; DB 12; Length 264;		
Best Local Similarity	35.2%; Pred. No. 2.2e-07;		
Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;			
OY 125 PATPATQAGNALPLLPQEFPEVYPLNTIGCANFTTRLSCTICYEEDTMAMFSGRHYYPT	184		
DB 36 PVSPLPAAQ-GIPLPQOLTKRSNAPVHIDVGHHYTSLSLATLTKYPPSRISRLNGTEPYTL	94		
OY 185 DS-BGRYVIFDRDGTAFRGVNLNFRSGDLPFRBRVR--AVYEAQYVAIGPLLEQLENWQ	240		
DB 95 DSLKHHYIFDRDGEIFRYYLSLSTRISKLLLPDDEFDSLIYEANYTOLQPVRELERWQ	154		
OY 241 PLKGEKVR 248			
DB 155 QOEQRRR 162			
RESULT 8			
US-10-024-579-10			
/ Sequence 10, Application US/10024579			
/ Patent No. US20020119522A1			
GENERAL INFORMATION:			
APPLICANT: Friddele, Carl Johan			
APPLICANT: Gerhardt, Brenda			
APPLICANT: Hilbun, Erin			
APPLICANT: Turner, C. Alexander Jr.			
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related			Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same			
FILE REFERENCE: LEX-0274-USA			
CURRENT APPLICATION NUMBER: US/10/024, 579			


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: CURRENT FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: US 60/258,595
: PRIOR FILING DATE: 2000-12-28
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 283
: TYPE: PRT
: ORGANISM: homo sapiens
: US-10-024-579-10

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Query Match	9.8%	Score 174.5	DB 12	Length 283
Best Local Similarity	35.2%	Pred. No. 2.4e-07		
Matches 45; Conservative	28	Mismatches 50	Indels 5	Gaps 3

[illegible]

QY	241	PLKGEKVR	248
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Db	155	QEQEQRRR	162

RESULT 9
US-09-764-864-1240

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: Patent No.: US20020132753A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Rosen et al.
:
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
:
: FILE REFERENCE: PRT23
:
: CURRENT APPLICATION NUMBER: US/09/764,864
:
: CURRENT FILING DATE: 2001-01-17
:
: Prior application data removed - consult PALM or file wrapper
:
: NUMBER OF SEQ ID NOS: 1792
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 1240
:

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1      title: test
2      ORGANISM: Homo sapiens
3      FEATURE:
4      NAME/KEY: SITE
5      LOCATION: (51)
6      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
7      NAME/KEY: SITE
8      LOCATION: (76)
9      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
10     NAME/KEY: SITE
11     LOCATION: (358)
12     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
13     US-09-764-864-1240
14
15 Query Match          8.8%; Score 157; DB 10; Length 378;
16 Best Local Similarity 29.4%; Pred. No. 1e-05;
17 Matches    68; Conservative   29; Mismatches   76; Indels    58; Gaps    12

```

```

QY      50  GCAAPGRRERVEGATATLPFHCHSPSPGCAAAARV-----MGAARARARGWVVYVYGGED- 105
Db      1  GGGPGCR-----YAAH--SGPGSGAMRVTLELNGSPKNGK-VVAYVGTLSDL 46
QY      106 ---SKRGGAMSS-----DAED-----FLEPATPTTQAGHAPL 133
Db      47  LSAASKIGATATSYNKGGLIDIALIXDDVLEWCEGEPTIDPQDSAPPEG----- 101b

```

```

OY      140 LPQEPFVPLNIGGAFTTRKLTLCIE-DYMAAMF--SGRHYIPTDSERYFIDRDG 1368
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      102 LAGFHDMGLTNVGRFTTTRSTLVNKRPSDMAAMFKKQGWGSKNQDHRALFIDRSP 161

```

```

QY 197 THEGVLNPLRSGLDPPREKVR--AVYKEAYYAIGPLLEQL-----NMQP 2411
      :|:::| | | : : |:::| | | | |
DB 162 EYFEPILNYLRHGQLIYVNDGINLGLVLEAREFGIDSLIEHLEVAIKNSQP 2122

```

RESULT 10
US-10-024-579-2
; Sequence 2, Application US/10024579
; Patent No. US20020119522A1

. APPLICANT: Friddle, Carl Johan
 . APPLICANT: Gerhardt, Brenda
 . APPLICANT: Hilbun, Erin
 . APPLICANT: Turner, C. Alexander Jr.
 . TITLE OF INVENTION: No. US20020119522a1el Human Ion Channel-Related Proteins
 . TITLE OF INVENTION: and Polynucleotides Encoding the Same
 . FILE REFERENCE: LEX-0274-USa
 . CURRENT APPLICATION NUMBER: US/10/024,579
 . CURRENT FILING DATE: 2001-12-18
 . PRIOR APPLICATION NUMBER: US 60/258,595
 . PRIOR FILING DATE: 2000-12-28

```

; SEQ ID NO 2
; LENGTH: 213
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-2

```

Qy	146	EVP	P	N	I	G	A	F	T	T	R	I	S	T	L	R	C	E	D	T	M	A	A	F	S	G	H	I	P	T	D	S	-----	G	R	I	P	I	D	R	O	G	H	F	G	2000			
Db	5	E	L	V	I	N	V	G	K	I	T	T	R	E	S	T	I	K	O	P	A	S	R	L	R	M	L	D	G	-----	D	O	E	F	K	M	V	G	O	I	F	D	R	O	G	L	L	S	59

```

OY 201 DVYNFLRSGD-LPPRE--RVRAYKKAQYIYAIGPLLEOLEN--KOP 241
      :|:|:|: | | | :|:|:|: | | :|:|
Db 60 FIDDFLRTHQLLPTEESDYLRIGREALFYEELRSLVDLLNPYLLQP 1055

```

RESULT 11
US-10-062-879-4
; Sequence 4, Application US/10062879
; Patent No. US20020127649A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Cockett, Mark I.
3  APPLICANT: Dilke, Daniel W.
4  APPLICANT: Chang Ling, Hui-Li-Ping
5  APPLICANT: Sokol, Patricia T.
6  TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
7  TITLE OF INVENTION: Polypeptides and Uses Thereof
8  FILE REFERENCE: ahp-98089
9  CURRENT APPLICATION NUMBER: US/10/062,379
10 CURRENT FILING DATE: 2002-01-31
11 PRIOR APPLICATION NUMBER: US/09/178,103
12 PRIOR FILING DATE: 1998-10-23
13 NUMBER OF SEQ ID NOS: 4
14 SOFTWARE: PatentIn Ver. 2.0

```

Query Match: 7.1%; Score 127; DB 12; Length 636;
 Best Local Similarity 34.7%; Pred. No. 0.0065;
 Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

```
QY 137 LPLP---QEPEVVPINIGGAHFTTRTSLRCYEDTMAAFSGAHYIPDSEGRYET 19
      :| | : |::| | | | | | | | | | : : : : | |
Db 27 MPLAPADKNKRODELIYVNSGRGFQWRTTLERPDTLGS--TEKEFFFNEDTKETFF 84
```


A:Cross-references: EMBL:U03263; PDB:1CMA21638.1, GSPDB:GN00020; CESP:F18A11.5
A:Experimental source: clone Y3871A
C:Genetics:
A:Gene: CESP:F18A11.5
A:Map position: 2
A:Introns: 7/3; 44/3; 99/3; 152/2; 198/3; 223/1

Query Match	8.1%	Score 143.5	DB 2	Length 373
Best Local Similarity	43.2%	Pred. No. 0.0033		
Matches 41, Conservative	12	Mismatches 33	Indels 9	Gaps 5

```
OY      146 EVVPLNIGGAHFTTILSTLRCEYEDTLMAAFSRRHYIPIDSEGRFIDRGTHFGVLNF   205
          | | :| | | :| | | :| | | | | | | | | | | | | | | | | | | |
Db       20 ERYLLNVGKKEFTTVATLIRVSDFVALMWSBRW--KTGE--IFDRDPKHFGKLVNY   75
```

DY 206 LRSGD--LPP-RERVRAYKEAQYYAIGPLEEQI 236
 ||||| :||| :|| ::
DB 76 LRDGDHFAVPSDTACDELRKAHFYNM-PLTAEIM 109

RESULT 7
T26019
hypothetical protein VM106r.1 - *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-19999
C:Accession: Z26019
R:Barlow, K.
Submitted to the EMBL Data Library, August 1998
Database accession number: Z26019

A;Accession: T26019
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecular function: not known

A1:Cross-references: EMBL:AL031266; PIDN:CAA20329.1; GSPDB:GN00020; CESP:VM106R.1
A1:Experimental source: clone VM106R

A;Gene: CESP:VM106R.1
A;Map. position: 2
A;Introns: 131/1

Query Match	8.0%	Score 143	DB 2	Length 190
Best Local Similarity	36.1%	Pred. No. 0.0015		
Matches 39	Conservative 18	Mismatches 39	Indels 12	Gaps 3

```
Oy      146 EVVPLNIGAHFTTRSLTLCREYEDTMAMFSG-----RHYIPDSEGRYIDRGTHF 199
       :|: ||::|| |  ||  ||::||: ||  : |: | ||::| |
Db      6 DVTLLNVGGMYTTTRSTLSKETDTILLANIASLSLSEDOANVTYLPDGILFVDRCGLP 65
```

```

QY      200 GDVLFNLRSGDLPFRERAVRYK---EAQYYAI---GPILLEQLENNQP 241
      111111: 1 1: 1 1: 11: 1: 11
Db      66 AYVLAHFLRTDKLSLPEQFREVAVRLKDEADFYRLERFSTLLSNASSISP 113

```

RESULT 8
T25972

C:Accession: T25972
C:Date: 15-Oct-1999 #sequence.revision 15-Oct-1999 #t

R: Wu, X.; Kramer, J.
submitted to the EMBL Data Library, December 1996
A: Description: The sequence of C. elegans cosmid ZC239
A: Reference number: Z20117

A/Accession: T25972
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Restrictions: 1-204 (EMM)

A: Cross-references: EMBL:U80884.2; PIDN:AB37944.1; GSPDB:GN00020; CESP:ZC239.5
 B: Experimental source: strain Bristol N2; clone ZC239
 C: Genetics:
 D: Gene: C89P.ZC330.5
 E:

A;Map position: 2
A;Introns: 38/3; 115/3; 135/1

Query Match	7.7%;	Score 137.5;	DB 2;	Length 204;
Best Local Similarity	30.5%;	Pred. No. 0.0043;		
Matches 40;	Conservative 21;	Mismatches 47;	Indels 23;	Gaps 6;

OY		. 147 VPEINIGGAHFTTRJSTLRCEYDTMLAMFSGRHYPPTSEGR----	YEFDRODGTREGD	201
		:: :::: : :	:	
Dd		5 IIKNVGMEESTENTL-----TKFECHPKOKLKFRKGINOTTFLEIDRSPTHEI	55	

```

Oy 202 VNFELRSG--DLPPR-ERVRAVYKEAOYYAIGPILLEQLEN-MQPIKGEKVQAFLGLMPY 257
      :|:|:| | | | : : :|:|:| | | | : | | | | | :|:|
Db 56 IANFMRDGKVDLPETLKLMPIFRETEYTTLASLVEQCGAIALSLGGPEPDKFRGRTIP 114

```

Oy	258	YKDHLERIVEI	268
		:	
Db	115	----TEAVVSI	121

RESULT 9
T25973

C:Accession:	C:Date:	C:Species:	C:Protein:	C:Accession:	C:Date:	C:Species:	C:Protein:
T25973	15-Oct-1999	<i>Caenorhabditis elegans</i>	hypodermal protein 20257.4	T25973	15-Oct-1999	<i>Caenorhabditis elegans</i>	hypodermal protein 20257.4

submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid ZC239.
A;Reference number: Z20117

A:Accession: 1259/3
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <MW>

A:Gene: CESP:ZC239.4
A:Cross-references: EMBL:U080842; PIDN:AAH37941.1; GSPDB:GN00020; CESP:ZC239.4
A:Experimental source: strain Bristol N2; clone ZC239
C:Genetics:

A;Map position: 2
A;Introns: 37/3; 133/3; 175/1
C;Superfamily: Caenorhabditis

Query Match	7.5%;	Score 134;	DB 2;	length 208;
Best Local Similarity	38.3%;	Pred. No. 0.008;		
Matches	36;	Conservative	12;	Mismatches 42;
			Indels	4;
			Caps	3

QY 146 EYVPLNIGGAHETTRSTLRCEDEDTMLAMFSGNHYIPDSEGRFIDRDGHHFGVLANF 205
 | | | : | | | | : | | | | | : | | |
 Db 3 EAVKLDVGGTIFKTSKSTLRF-DGFFPTMLGSGIGLVNDESGCIFIDRSPKHFLLINF 61

```

OY 206 LRSG--DLPPRR-VRAVYKKAQYYAIGPLLEQL 236
      :| | | : |||| : :||
Db 62 MRDGLALPKNERDTELMAAEQYYLLDGLIDRL 95

```

RESULT 10
T32070

C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T32070

submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F22E5
A:Reference number: Z21119

Accession: J22070
 A:Status: preliminary; translated from GH/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-231 <GRA>

A:Accession: EMBL:AC010001, F:UN:AMB001/1, G:SPDB:5N000420, C:Genetics: Experimental source: strain Bristol N2, clone F22E5
 C:Gene: CESP:F22E5.6
 C:Gene: CESP:F22E5.6

A;map position: 2
A;introns: 40/3; 125/3; 170/1

Page 3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC339.12

Query Match 7.48; Score 134; DB 2; Length 231;

Best Local Similarity 39.48; Pred. No. 0.0092;

Matches 37; Conservative 10; Mismatches 41; Indels 6; Gaps 3;

QY 146 EVPLNIGGAFTTRLSLRCYE--DTMLAMFSGRHYPIDSGRYFIDRDGTHFGVNL 205

DB 6 EKILNIGGTFETSKSLTKF-DSEFKTLLETIPIDKDSNCFIDRSPRFEKILNT 64

QY 206 LRSG--DLPP--RRVRAVYKEAOYAIQPLLE 234

DB 65 LRSGADVDLPESEKEREKAEKAEQFLLGLE 98

RESULT 11

hypothetical protein ZC339.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25976

R:Wu, X.; Kramer, J.

A:Description: The sequence of C. elegans cosmid ZC339.

A:Reference number: Z20117

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-140 <NUC>

A:Cross-references: EMBL:U08042; PIDN:AA37956.1; GSPDB:GN00020; CESP:ZC339.14

A:Experimental source: strain Bristol N2; clone ZC339

C:Genetics:

A:Gene: CESP:ZC339.14

A:Map position: 2

A:Intons: 37/3; 132/1

Query Match 7.48; Score 132.5; DB 2; Length 140;

Best Local Similarity 34.98; Pred. No. 0.0063;

Matches 38; Conservative 19; Mismatches 41; Indels 11; Gaps 5;

QY 146 EVPLNIGGAFTTRLSLRCYE--DTMLAMFSGRHYPIDSGRYFIDRDGTHFGDV 202

DB 3 EVPLDVGTFETSKSLTKFNGFFKTMLECDIG---LKIDESCIFIDRSPKHFDTL 58

QY 203 LNFRLSGD--LPRE--RVRAVYKEAOYAIQPLLEOLEN-MOPLKEKY 247

DB 59 LNFRLDGDVALPNCLEKELVLEQFLLDGLIEMCNKINPVEPKL 107

RESULT 12

hypothetical protein C40A11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000

C:Accession: T25976

R:Wu, X.; Goela, D.

A:Description: The sequence of C. elegans cosmid C40A11.

A:Reference number: Z21374

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-179 <MAG>

A:Cross-references: EMBL:AF099914; PIDN:AA66757.1; GSPDB:GN00020; CESP:C40A11.6

A:Experimental source: strain Bristol N2; clone C40A11

C:Genetics:

A:Gene: CESP:C40A11.6

A:Map position: 2

A:Intons: 40/3; 123/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC339.12

Query Match 7.48; Score 132; DB 2; Length 179;

Best Local Similarity 36.88; Pred. No. 0.0093;

Matches 39; Conservative 21; Mismatches 36; Indels 10; Gaps 6;

QY 147 VPLNIGGAFTTRLSLRCYE--DTMLAMFSGRHYPIDSGRYFIDRDGTHFGVNL 206

DB 7 IVKLNVGSEVETWKSSTL-TKODGFFKTLIENNVVKKDTSQCYTIDRSPKFEVLYNM 65

QY 207 RSG--DLPPRR--RVRAVYKEAOYAIQPLLEOLEN-QPLKEKY 248

DB 66 RSGVTVPDSEKELQELKEAEFY--LLEHLVDLCEPIK-NKIR 106

RESULT 13

hypothetical protein T23B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32221

R:Davidson, S.; Wohldmann, P.; Giliam, B.

A:Description: The sequence of C. elegans cosmid T23B12.

A:Reference number: Z21137

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-670 <NAV>

A:Cross-references: EMBL:AF022982; PIDN:AA66932.1; GSPDB:GN00023; CESP:T23B12.6

A:Experimental source: strain Bristol N2; clone T23B12

C:Genetics:

A:Gene: CESP:T23B12.6

A:Map position: 5

A:Intons: 87/2; 185/3; 293/1; 400/1; 457/1; 540/2; 635/3

Query Match 7.48; Score 132; DB 2; Length 670;

Best Local Similarity 31.28; Pred. No. 0.05;

Matches 35; Conservative 20; Mismatches 55; Indels 2; Gaps 2;

QY 147 VPLNIGGAFTTRLSLRCYE--DTMLAMFSGRHYPIDSGRYFIDRDGTHFGVNL 206

DB 20 IVNVLGGRATSCNTLWIPDSFFSLSGRNVSXKDPGATIDRDGTHFGVNL 79

QY 207 RSGDLP--PREVRAVYKEAOYAIQPLLEOLEN-MOPLKEKY 248

DB 80 RTKQVLDGCIKVDLKHLEALFGLPLIRLTLCELSSTGSGVYFCGMP 131

RESULT 14

hypothetical protein ZC339.15 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T25978

R:Wu, X.; Kramer, J.

A:Description: The sequence of C. elegans cosmid ZC339.

A:Reference number: Z20117

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-246 <NUC>

A:Cross-references: EMBL:U08042; PIDN:AA37955.1; GSPDB:GN00020; CESP:ZC339.15

A:Experimental source: strain Bristol N2; clone ZC339

C:Genetics:

A:Gene: CESP:ZC339.15

A:Map position: 2

A:Intons: 37/3; 127/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC339.12

Query Match 7.48; Score 131.5; DB 2; Length 246;

Best Local Similarity 30.28; Pred. No. 0.015;

Matches 42; Conservative 27; Mismatches 49; Indels 21; Gaps 6;

QY 146 EVPLNIGGAFTTRLSLRCYE--DTMLAMFSGRHYPIDSGRYFIDRDGTHFGDV 202

Db 3 ETVKIDVCGTIFKTSRSLTFKNGFFKTMLESIDG----LKIDSGSIFIDNSPKNFDLI 58
 QY 203 LNFIRSGD--LPRE-RVRAVKEAQAIAIGPLLEOLEN-MQPLKGEKYROAFLGLMPY 258
 Db 59 LNFMRDGDVLPNCELEKKELEVEAQLDGLIELCNSKIELEVAEPRKIKLR-----111
 QY 259 KDHLERIVEIARLRAVORK 277
 Db 112 --IESDEQFLQILAVOOK 127

RESULT 15

T33592

hypothetical protein C40A11.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

C:Accession: T33592

R:Magyl, L.; Goela, D.

Submitted to the EMBL Data Library, October 1998

A:Description: The sequence of C. elegans cosmid C40A11.

A:Reference number: 221374

A:Accession: T33592

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-220 <NAC>

A:Cross-references: EMBL:AF09914; PIDN:AAC68762.1; GSPDB:GN00020; CESP:C40A11.7

A:Experimental source: strain Bristol N2; clone C40A11

C:Genetics:

A:Gene: CESP:C40A11.7

A:Map position: 2

A:Insertions: 40/3; 123/3; 162/1

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 7.4%; Score 131; DB 2; Length 220;

Best Local Similarity 31.1%; Pred. No. 0.014;

Matches 42; Conservative 26; Mismatches 45; Indels 22; Gaps 7;

QY 147 VVPINIGGAHTTIRLSTRCYEDTMLAMFSGRAHYIPDSEGRYFIDRDGTHFGDVLNFI 206
 Db 7 IVKLNVGSGVFEFTWKSTL-TKODGFFKTLVEETINIPVKKDTSQYFIDRSRPFYEVLYNFM 65
 QY 207 RSG--DLPRE-RVRAVKEAQAIAIGPLLEOLEN-MQPLKGEKYROAFLGLMPYKDH 262
 Db 66 RSGVTVLPDSSEKELEKEAEFY---LLEQLVDLCERINNO-----INTYRSSH- 112
 QY 263 ERIVEIARLRAVORK 277
 Db 113 ----ELQIITASTKK 123

Search completed: February 12, 2003, 11:09:01
 Job time : 23 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: February 12, 2003, 11:06:15 / Search time 34 Seconds
(without alignments)
2078.652 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780
Sequence: 1 MTAVALNRKSGKGPLRRRP.....NNEKSPYQLPAGVFQHEWG 343

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	981	55.1	289	4	Q96MP8
2	584	32.8	214	6	Q9BE68
3	274	15.4	225	4	Q9B013
4	245.5	13.8	290	11	Q9CU79
5	244	13.7	234	11	Q8R3T6
6	211.5	11.9	228	4	Q8RCA6
7	208	11.7	315	11	Q922M3
8	206	11.6	310	4	Q96SU0
9	206	11.5	313	4	Q9H3F6
10	204	11.5	329	4	Q9GSA1
11	204	11.2	329	4	Q8WZ19
12	200	11.0	301	5	Q18986
13	196	10.8	329	5	Q9V9F4
14	193	10.8	333	4	Q8WUN2
15	192.5	10.8	338	5	Q9WZF9
16	189.5	10.6	338	5	Q9WZF9

17	180.5	10.1	228	5	Q9VDH3	Q9VDH3 drosophila
18	180	10.1	298	10	Q9SE95	Q9SE95 arabidopsis
19	180	10.1	707	4	Q8WY93	Q8WY93 homo sapien
20	180	10.1	707	4	Q8TBC3	Q8TBC3 homo sapien
21	177.5	10.0	259	11	Q9CYK4	Q9CYK4 mus musculus
22	176	9.9	704	11	Q9ES31	Q9ES31 mus musculus
23	174.5	9.8	283	4	Q9BS11	Q9BS11 homo sapien
24	174.5	9.8	730	5	Q9VH62	Q9VH62 drosophila
25	172	9.7	316	11	Q70479	Q70479 mus musculus
26	170.5	9.6	259	4	Q8WYF5	Q8WYF5 homo sapien
27	170.5	9.6	259	11	Q9D7X1	Q9D7X1 mus musculus
28	168.5	9.5	234	4	Q9BV16	Q9BV16 homo sapien
29	165	9.3	815	4	Q9Y5V7	Q9Y5V7 homo sapien
30	165	9.3	815	4	Q8WX16	Q8WX16 homo sapien
31	164.5	9.2	234	4	Q9GN73	Q9GN73 homo sapien
32	163.5	9.2	435	4	Q9P2M9	Q9P2M9 homo sapien
33	159	8.9	247	4	Q96G52	Q96G52 homo sapien
34	159	8.9	290	4	Q9S517	Q9S517 homo sapien
35	152.5	8.9	325	4	Q96CX2	Q96CX2 homo sapien
36	152.5	8.6	234	11	Q9VC57	Q9VC57 mus musculus
37	150.5	8.5	276	5	Q16706	Q16706 caenorhabditis
38	147	8.3	234	4	Q9NXV2	Q9NXV2 homo sapien
39	146.5	8.2	647	4	Q9HSA2	Q9HSA2 homo sapien
40	146.5	8.2	647	4	Q75671	Q75671 homo sapien
41	146.5	8.2	651	11	Q03719	Q03719 mus musculus
42	144.5	8.1	212	5	Q16613	Q16613 caenorhabditis
43	143.5	8.1	373	5	Q9XWL7	Q9XWL7 caenorhabditis
44	143	8.0	190	5	Q9XKA3	Q9XKA3 caenorhabditis
45	139.5	7.8	632	13	Q8UW33	Q8UW33 gallus gallus

ALIGNMENTS

RESULT 1

Q96MP8 PRELIMINARY; PRT; 289 AA.
ID Q96MP8
AC Q96MP8;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 20, Last annotation update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CDNA FLJ32069 f1s, clone OCBF100018, weakly similar to tumor necrosis factor, alpha-induced protein 1, endothelial.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Osima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Mueshino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagauma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T., "NEBO human cDNA sequencing project", submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AK056631; BAB71236.1;
DR InterPro; IPR003131; K.tetra.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02214; K.tetra; 1.
DR SMART; SM00203; TK; 1.3132 MW; 1FDD1F618CD5E459 CRC64;
SQ SEQUENCE 289 AA; 33132 MW; 1FDD1F618CD5E459 CRC64;

Query Match 55.1%; Score 981; DB 4; Length 289;

Best Local Similarity 100.0%; Pred. No. 1.7e-66; Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 MYVTGTRPDSRQDGAMSSDAEDDFLEPATPTATGAGHAPLPLPDPFPPVPLNTGGA 155
DB 1 MYVTGTRPDSRQDGAMSSDAEDDFLEPATPTATGAGHAPLPLPDPFPPVPLNTGGA 60

QY 156 HETRLSTLRCYEDTMTAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNLFRSGDLPPRE 215
 DB 61 HETRLSTLRCYEDTMTAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNLFRSGDLPPRE 120
 QY 216 RYRAYKKAQYVAIGPLLEQLENNOPKGEKVRQAFLGIMPYKDLERIVETARLRAVQ 275
 DB 121 RYRAYKKAQYVAIGPLLEQLENNOPKGEKVRQAFLGIMPYKDLERIVETARLRAVQ 180
 QY 276 RYRAYKKA 284
 DB 181 RYRAYKKA 189

RESULT 2

Q9BE68 PRELIMINARY: PRT: 214 AA.
 AC 09BE68: PRELIMINARY: PRT: 214 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 25.0 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 CX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL LOBE LEFT;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terno K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length clones from macaque brain cDNA
 RT libraries."
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB056802; BAB39326.1;
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 KW Hypothetical protein.
 SO SEQUENCE 214 AA; 25001 MW; FBD124AB711EB85 CRC64;

Query Match 32.8%; Score 584; DB 6; Length 214;
 Best Local Similarity 99.1%; Pred. No. 1.3e-36;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 171 MAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNLFRSGDLPPREYRAYKKAQYVAIG 230
 DB 1 MAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNLFRSGDLPPREYRAYKKAQYVAIG 60
 QY 231 PLEQLENNOPKGEKVRQAFLGIMPYKDLERIVETARLRAVQRYAYKKA 284
 DB 61 PLEQLENNOPKGEKVRQAFLGIMPYKDLERIVETARLRAVQRYAYKKA 114

RESULT 3

Q9B013 PRELIMINARY: PRT: 225 AA.
 AC 09B013: PRELIMINARY: PRT: 225 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Unknown (protein for MGC:3993) (protein for MGC:12376).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 SO SEQUENCE FROM N.A.

RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC001929; AAH01929.1;
 DR EMBL; BC001062; AAH01062.1;
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 DR SMART: SM00225; BTB; 1.
 SO SEQUENCE 225 AA; 26188 MW; BA8435C5D6C2476D CRC64;

Query Match 15.4%; Score 274; DB 4; Length 225;
 Best Local Similarity 45.7%; Pred. No. 4e-13;
 Matches 59; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 147 VPLNIGAHFTRLSTLRCYEDTMTAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNL 206
 DB 4 VPLNIGAHFTRLSTLRCYEDTMTAAFGSRHYIPDSEGRYFIDRGTGTFGVDLNL 63
 QY 207 RSGDLPPREYRAYKKAQYVAIGPLLEQLENNOPKGEKVRQAFLGIMPYKDLERIV 265
 DB 64 RTGVY-PROHIDPEYREARQFYKIPKLVKLEMDPQIFGSEYVRKQPLQVPSSENLELM 122
 QY 266 VEIARLRAV 274
 DB 123 VEIARLRAV 131

RESULT 4

Q9C079 PRELIMINARY: PRT: 290 AA.
 AC 09C079: PRELIMINARY: PRT: 290 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 3430433B02R1K protein (fragment).
 GN 3430433B02R1K.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kouchiwa H.,
 RA Kuehl P., Lewis S., Matano Y., Ninkaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzeroli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz G., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK017384; BAB30722.1;
 DR MGD; MGI:1918643; 5430433B02R1K.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 DR SMART: SM00225; BTB; 1.
 FT NON_TER 1
 SO SEQUENCE 290 AA; 31443 MW; 1AB511251CEBDD005 CRC64;

Query Match 13.8%; Score 245.5; DB 11; Length 290;
 Best Local Similarity 28.7%; Pred. No. 8e-11;
 Matches 93; Conservative 37; Mismatches 103; Indels 91; Gaps 12;

QY 16 LRRRLPALPRLGLPLPANGG--TSASASGSRSGCAPAGHERGVGATLPAHCL 73
 DB 1 LRRR---RPRRAGAAATPGSGSLVPSAAAAAATAAAAGR-----GLRPRARAL 50
 QY 74 SPSPGQPAAGVMPGAPRARGVVTGREGPSRQDGMSSSDADDFLEPATPTATQA 133
 DB 51 GPPAS-----PG--RVASALVQY-----PRLSSSDAYLEQDNG-----DW 85
 QY 134 GHALPLPEPPEVPLNIGAHFTTRSLTLCYEDTMLAAMFSGHHYIPTDSEGRYFID 193
 DB 86 GYMM-----SDPYTLNVGHLVYTTSLTLTRYPDSMLGAMFGDFPPARDPQGNVFID 138
 QY 194 RDGHFEGVNLFRSGDLP---PRERVAVYKEAQYTAIGPLLEQENMOPKGEKYRQA 250
 DB 139 RDGPLFRVYVNLFRSELTLPLDFKEFDLRKADFTQIEPLIOCLNDPRPL----- 190
 QY 251 FLGLMPYKDLHERIVEIARLAVORRKA-----FAKLKSL----- 286
 DB 191 -----YMDFFEEVVELSSTRKLSKSNPVAVITTLQTLTTKVSHLSIGISNYFTKMK 244
 QY 287 -----TPSWLMSVLIKMPPGVTS 304
 DB 245 HMMPEFASLHLMTVTRIPGSLIS 268

RESULT 5

Q8R3T6 ID 08R3T6 PRELIMINARY; PRT; 234 AA.

AC 08R3T6;
 DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
 DE Similar to hypothetical protein MGC2376.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC024588; AAH24588.1;
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 27008 MW; F727A35094F516FA CRC64;

Query Match 13.7%; Score 244; DB 11; Length 234;
 Best Local Similarity 41.2%; Pred. No. 7.9e-11;
 Matches 56; Conservative 34; Mismatches 40; Indels 6; Gaps 4;

QY 146 EYVPLNIGAHFTTRSLTLCYEDTMLAAMF--SGHHYIPTDSEGRYFIDRDGTHFGDVL 203
 DB 18 KYVELNVGGOFTYTMGTLMKHPGSKFSSEILSRARHY--KDAQGFPIIDRPGYFGLL 75
 QY 204 NPLRSGDLPERRRVARVYKEAQYTAIGPLLEQENMOPKGEKYRQAFTGLMPYKDL 262
 DB 76 DILRIGVY-PTIYVPEVYQZAKFTQIHLVTKLIEDPQIFGEQVARTQFLMGVFNRENT 134
 QY 263 ERIVEIARLAVORRKA 278
 DB 135 EYVHLARARAVAMRS 150

RESULT 6

Q8TCA6 ID 08TCA6 PRELIMINARY; PRT; 228 AA.

AC 08TCA6;
 DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)

DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Hypothetical 26.5 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

QY 148 VPLNIGAHFTTRSLTLCYEDTMLAAMFSGHHYIPTDSEGRYFIDRDGTHFGDVLNFLR 207
 DB 5 VTLNVGHLVYTTSLTLTRYPDSMLGAMFGDFPPARDPQGNVFIDRDGTHFGDVLNFLR 64
 QY 208 SGDLP---PRERVAVYKEAQYTAIGPLLEQENMOPKGEKYRQAFTGLMPYKDLHER 264
 DB 65 TSELTLPLDFKEFDLRKADFTQIEPLIOCLNDPRPL-----YMDTFEE 110
 QY 265 IVEIARLAVOR 276
 DB 111 VVELSTRKLSK 122

Query Match 11.9%; Score 211.5; DB 4; Length 228;
 Best Local Similarity 38.6%; Pred. No. 2.2e-08;
 Matches 51; Conservative 19; Mismatches 45; Indels 17; Gaps 2;

QY 148 VPLNIGAHFTTRSLTLCYEDTMLAAMFSGHHYIPTDSEGRYFIDRDGTHFGDVLNFLR 207
 DB 5 VTLNVGHLVYTTSLTLTRYPDSMLGAMFGDFPPARDPQGNVFIDRDGTHFGDVLNFLR 64
 QY 208 SGDLP---PRERVAVYKEAQYTAIGPLLEQENMOPKGEKYRQAFTGLMPYKDLHER 264
 DB 65 TSELTLPLDFKEFDLRKADFTQIEPLIOCLNDPRPL-----YMDTFEE 110
 QY 265 IVEIARLAVOR 276
 DB 111 VVELSTRKLSK 122

RESULT 7

Q922M3 ID 0922M3 PRELIMINARY; PRT; 315 AA.

AC 0922M3;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DE Similar to tumor necrosis factor, alpha-induced protein 1
 (endothelial).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC006935; AAH06935.1;
 DR InterPro: IPR000210; Pfam: PF02.
 DR InterPro: IPR003131; K.tetra.
 DR Pfam: PF02214; K.tetra; 1.
 DR PROSITE; PS50097; BTB; 1.
 SQ SEQUENCE 315 AA; 35701 MW; 590AEF2D4E22D2D9 CRC64;

Query Match 11.7%; Score 208; DB 11; Length 315;
 Best Local Similarity 32.9%; Pred. No. 6.2e-08;
 Matches 54; Conservative 16; Mismatches 48; Indels 46; Gaps 4;

QY 77 SGQPAAGVMPGAPRARGVVTGREGPSRQDGMSSSDADDFLEPATPTATQA 136
 DB 5 SGDSVSSAVPAAARTTSF---KGASPSK----- 32
 QY 137 LPLPQEPPEVPLNIGAHFTTRSLTLCYEDTMLAAMFSGHHYIPTDSEGRYFIDRDG 196
 DB 33 -----YKLVNAGLVTYTTMOTL-TKQDTMLKAMSGMEVLTDSGWLIDRCG 81
 QY 197 THFGDVLNFRSGDLP---PRERVAVYKEAQYTAIGPLLEQ 237
 DB 82 KHFGIIVNIRDGVPLPESRREIEELADAKYIVLVGGLLEBO 125

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RESULT 8
ID 096S00 PRELIMINARY; PRT; 310 AA.
AC 096S00;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DE 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, last annotation update)
DE CCNA FLJ14637 fls, clone NT2R2001327, moderately similar to tumor
DE necrosis factor, alpha-induced protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Isoget T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK027543; BAB5188.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR PROSITE: PS50097; BTB; 1.
SQ SEQUENCE 310 AA; 35042 MW; BA79F680F6920CF CRC64;

Query Match 11.6%; Score 206; DB 4; Length 310;
Best Local Similarity 32.3%; Pred. No. 8.6e-08;
Matches 53; Conservative 18; Mismatches 47; Indels 46; Gaps 4;

QY 77 SGPAGAGVMPGARRAGVYVGTGREPDSRRQDAMSSSDAEDDFLEPATPTAQGHA 136
DB 2 SGEVSSAVPAATRTTSF---KGTSPSK----- 29
QY 137 LPLPQEPPEVVPINIGAHFTTRISTRCYEDTMLAMFSGRHYIPDSEGRYFIDRG 196
DB 30 -----YVKLVGALYTTMQTL-TKODTLMKMFSGRMEVLTPESEGWILDRG 78
QY 197 THEGDVNLFLNSGDLF---PRERVAAYKEAQYVAIGPLLEOLE 237
DB 79 KHEFTILNLYLDGAVLPESRREIELLAERKYVVOGLVEECQ 122

RESULT 9
ID 09H3F6 PRELIMINARY; PRT; 313 AA.
AC 09H3F6;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, last annotation update)
DE MSTR028.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hul R.T.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF113308; AAG39279.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
SQ SEQUENCE 313 AA; 35432 MW; 199AF07A30D5BCA6 CRC64;

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Query Match 11.6%; Score 206; DB 4; Length 313;
Best Local Similarity 32.3%; Pred. No. 8.7e-08;
Matches 53; Conservative 18; Mismatches 47; Indels 46; Gaps 4;

QY 77 SGPAGAGVMPGARRAGVYVGTGREPDSRRQDAMSSSDAEDDFLEPATPTAQGHA 136
DB 5 SGEVSSAVPAATRTTSF---KGTSPSK----- 32
QY 137 LPLPQEPPEVVPINIGAHFTTRISTRCYEDTMLAMFSGRHYIPDSEGRYFIDRG 196
DB 33 -----YVKLVGALYTTMQTL-TKODTLMKMFSGRMEVLTPESEGWILDRG 81
QY 197 THEGDVNLFLNSGDLF---PRERVAAYKEAQYVAIGPLLEOLE 237
DB 82 KHEFTILNLYLDGAVLPESRREIELLAERKYVVOGLVEECQ 125

RESULT 10
ID 096SAL PRELIMINARY; PRT; 329 AA.
AC 096SAL;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, last annotation update)
DE TNFAIP1-like protein.
GN FKSG86.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Wang Y.-G., Gong L.;
RT "Cloning and characterization of FKSG86, a novel gene encoding a
RT TNFAIP1-like protein."
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY027918; AAK27301.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR PROSITE: PS50097; BTB; 1.
SQ SEQUENCE 329 AA; 36371 MW; 61092C2B0E81EA2D CRC64;

Query Match 11.5%; Score 204; DB 4; Length 329;
Best Local Similarity 41.2%; Pred. No. 1.3e-07;
Matches 56; Conservative 19; Mismatches 41; Indels 20; Gaps 7;

QY 123 LEPATPTATQAGHAL---PLLPQEPPEVVPINIGGA-HFTTRISTLRCYEDTMLAMFS 177
DB 16 LEAPKPSGLEPGAPAYGKPLTPNS--KYVKLVGSGSLHYTT-LRTL-TGODTLMKAFS 71
QY 178 GRHTIPDSEGRYFIDRGTHFGDYVNLFLNSGDLFPRERVAAYK---EAQYVAIGPLLE 234
DB 72 GRVEVLTDAGGVLIDSGRHFHTLNTLRDGSVPLPESTHELGLLEARYIVVOGLIE 131
QY 235 -----OLENMQPL 242
DB 132 DCQALQGRKRETSPL 147

RESULT 11
ID 08WZ19 PRELIMINARY; PRT; 329 AA.
AC 08WZ19;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, last annotation update)
DE Hypothetical 36.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289573; AML557.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
DR Hypothetical protein.
SQ SEQUENCE 329 AA; 36357 MW; 17A8AC2DBE81E78 CRC64;

Query Match 11.5%; Score 204; DB 4; Length 329;
Best Local Similarity 41.2%; Pred. No. 1.3e-07;
Matches 56; Conservative 19; Mismatches 41; Indels 20; Gaps 7;

QY 123 LEPAATPAAGAGAL---PLAQEPPEVVPINIGA-HFTTRISTLCYEDTMAMFS 177
DB 16 LEAPKPSGLEGPAAYGLKPLTPMS--KYVKLVNGSGSLHYTT-LRTL-TGDDTMKAMFS 71
QY 178 GRAYIPTDSEGRYFIDRDGTHFGDVLNFRSGDLPRERAVAYK---EAQYVAIPLE 234
DB 72 GRAYVITDAGGWLIDRSGHFGTILNLDGVSPLPESTRELEGLGEARYIVGLIE 131
QY 235 -----OLENNQPL 242
DB 132 DQALAQKRETLSP 147

RESULT 12
QY 018986 PRELIMINARY; PRT; 220 AA.
AC 018986;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DR 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE D2045.8 protein.
GN D2045.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP MEDLINE=99069613; PubMed=9851916;
RX SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL: Z55639; CAAG4696.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
SQ SEQUENCE 220 AA; 25651 MW; D4E755FBBF7D3296 CRC64;

Query Match 11.2%; Score 200; DB 5; Length 220;
Best Local Similarity 35.6%; Pred. No. 1.6e-07;
Matches 64; Conservative 22; Mismatches 46; Indels 48; Gaps 10;

QY 123 LEPAATPAAGAGALPLLPQEPPEVVPINIGA-HFTTRISTLCYEDTMAMFSGRAYI 182
DB 1 MERST-----IVKLDVGGKIFKTTIFIL-CKHDSKMTMCTDVPV 40

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QY 183 PMDSGRYFIDRDGTHFGDVLNFRSGD--LPRER-VRAYKENQYVAIPLEQENM 239
DB 41 TKNBSGVFIDRDKSRHRLINFLNRDQIALPDSRDREYLAASRLPLP----- 95
QY 240 OPLKGEKVRQAFGLMPYKDYKHLERIVEIARLVORAKAPAKLSLPSMLSVLTKMP 299
DB 96 --LCGERLDS---LNNY--HLVSTV---LEA--KRIIPATERPI-----VVKLP 135

RESULT 13
QY 09V9F4 PRELIMINARY; PRT; 301 AA.
AC 09V9F4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE CG10465 protein (NES7120p).
GN CG10465.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Finnkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borzova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Chidley E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu X., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iobagwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spieth E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guartin H., Krcmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

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RA. Celinker S.;
 RL. Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR. EMBL; AF003787; AAF57336.1; -
 DR. EMBL; AY071521; AAL49143.1; -
 DR. Flybase; FBgn0033017; CG10465.
 DR. InterPro; IPR000210; BTB_POZ.
 DR. InterPro; IPR003131; K_tetra.
 DR. Pfam; PF02214; K_tetra.1.
 DR. SMART; SM00225; BTB; 1.
 SQ. SEQUENCE 301 AA; 34048 MW; 4BEC3E6B70258F4 CRC64;

Query Match 11.0%; Score 196; DB 5; Length 301;
 Best Local Similarity 31.3%; Pred. No. 4.7e-07;
 Matches 62; Conservative 32; Mismatches 76; Indels 28; Gaps 6;

QY 139 LLPQEPPEVPLNIGAHFTRLSTLCYEDTMLAMFSGRHYPDSEGRFIDRGTH 198
 DB 12 LKNGHSGYLKLVNGGHLYTTIGTLTKNDYMLSMFSGRMVLDSDGWLIDRCGNH 71
 QY 199 FGDIYLFARSGDLR---PREHRYAYKKEQYVAIGPLGLE-----NMQP-----L 242
 DB 72 FGIILNYRDGTVPLEPNETKELAELEAKKYCITELAISCEALYAHDEPKRICRIPLI 131
 QY 243 KGEKVAFLGLMPYKNDHLERIVEIARLAVORAKARPAKLKSLTPSWLMSVLKMPGV 302
 DB 132 TSGKEQGLLSVS-----LKPAVILVYQROKNKSYSTSDNLK-NIELEDKL 180
 QY 303 TSWINAEERLYLEPDI 320
 DB 181 SLRFN-ERILFKIVIGP 197

RESULT 14

Q96P93 PRELIMINARY; PRT; 329 AA.

AC 096P93;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Polymerase delta-interacting protein 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21477421; PubMed-11593007;
 RA He H., Tan C.K., Downey K.M., So A.G.;
 RT "A tumor necrosis factor alpha- and interleukin 6-inducible protein
 RT that interacts with the small subunit of DNA polymerase delta and
 RT proliferating cell nuclear antigen."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:11979-11984(2001).
 DR EMBL; AF401315; AAL14962.1; -
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra.1.
 DR PROSITE; PS50097; BTB; 1.
 SQ SEQUENCE 329 AA; 36395 MW; D356490B48995187 CRC64;

Query Match 10.8%; Score 193; DB 4; Length 329;

Best Local Similarity 37.5%; Pred. No. 8.9e-07;
 Matches 51; Conservative 22; Mismatches 43; Indels 20; Gaps 6;

QY 123 LEPATPTATQAGHAL---PLLPQEPPEVPLNIGAHFTRLSTLCYEDTMLAMF 177
 DB 16 LEAPKPSGLPEGPAAYGLKPLFPNS--KYKLVNNGSLHYTLLITLNG--QDTMLKAMFT 71
 QY 178 GRHYITDSEGRFIDRGTHFDVNLFLASGDLPPRRERYAYK---EAQYVAIGPLLE 234
 DB 72 GRLEVLTGSGWVLTDRSGHFGTILNYLDGSSVLPPESTKEIGELLGEARYLYVQGLTE 131
 QY 235 -----OLENMQPL 242

DB 132 DCOLALQOKRETTLSPL 147

RESULT 15

Q8W0N2 PRELIMINARY; PRT; 333 AA.

AC 08W0N2;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 36.2 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CERVIX;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019929; AAL19929.1; -
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra.1.
 DR SMART; SM00225; BTB; 1.
 DR Hypothetical protein.1
 FT NON_TER
 SQ SEQUENCE 333 AA; 36219 MW; 657EB1B8167D5F6B CRC64;

Query Match 10.8%; Score 192.5; DB 4; Length 333;
 Best Local Similarity 30.2%; Pred. No. 9.9e-07;
 Matches 74; Conservative 28; Mismatches 98; Indels 45; Gaps 9;

QY 123 LEPATPTATQAGHAL---PLLPQEPPEVPLNIGAHFTRLSTL 164
 DB 36 LTASTOFTCHGSSAFSLSVSPVLPKISPPVSPSPSGPVLNMGTLSTLETL 95
 QY 165 RCYEDTMLAMFSGRHYP---TDSEGRYFIDRGTHFDVNLFLASG---DLPPRRERY 218
 DB 96 TRFDPSSMGAFRAGTTPPPNLSGGGHYFIDRGKAFRLNLRGLDLPFRGGET 155
 QY 219 AVYK-EAQYVAIGPLLENNQPKGEKVAFLGLMPYKNDHLERIVEI 269
 DB 156 ALIRAEADFYQIRPLDLRLREASGTPAPYA--ALHADVDVSPRLVHFSARGRPHY 213
 QY 270 RLRAVORAKARPAKLKSLTPSWLMSVLKMPGVTSWINAEERLYLETPIGPERONNEKS 329
 DB 214 ELSSVOVDFPANEFTDSECTSECIGALRARF--GYASGDRAEGSPHRLTEVAPR----- 263
 QY 330 PVQLP 334
 DB 264 FVELP 268

Search completed: February 12, 2003, 11:08:34
 Job time : 36 secs